# SCORE Search Results Details for Application 10591347 and Search Result 20110118_143603_seq2sub1624a.rng.

This page gives you Search Results detail for the Application 10591347 and Search Result 20110118_143603_seq2sub1624a.rng.

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                        GenCore version 6.3
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OM nucleic - nucleic search, using sw model

Run on:          January 18, 2011, 21:51:00 ; Search time 1435 Seconds
                                             (without alignments)
                                             50622.995 Million cell updates/sec

Title:           SEQ2SUB1624A
Perfect score:   3424
Sequence:        1 aggatcagaacaatgcctcc..........taaactagttcatttcaaaa 3424

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        18225500 seqs, 10608060480 residues

Total number of hits satisfying chosen parameters:      36451000

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       N_Geneseq_201023:*
            1:   geneseqn1:*
            2:   geneseqn2:*
            3:   geneseqn3:*
            4:   geneseqn4:*
            5:   geneseqn5:*
            6:   geneseqn6:*
            7:   geneseqn7:*
            8:   geneseqn8:*
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                   9:   geneseqn9:*
                                SUMMARIES
                      %
                      Query
Result             Match  Length  DB    ID                          Description
 No.     Score
------------------------------------------------------------------------------------
     1   3422.4    99.9    3424    1   AAS14365              Aas14365 cDNA enco
     2   3422.4    99.9    3424    1   ABL59523              Abl59523 Human pho
     3   3422.4    99.9    3424    2   ADE85076              Ade85076 Farnesyl
     4   3422.4    99.9    3424    4   ADZ00490              Adz00490 p110-beta
     5   3422.4    99.9    3424    4   AEH10445              Aeh10445 PIK3CA cD
     6   3422.4    99.9    3424    4   AED31618              Aed31618 cDNA (SEQ
     7   3422.4    99.9    3424    4   AEG93388              Aeg93388 Human tum
     8   3410.4    99.6    3412    1   AAQ51156              Aaq51156 Human p11
     9   3410.4    99.6    3412    4   AED31617              Aed31617 cDNA (SEQ
    10   3410.4    99.6    3423    3   ADU05935              Adu05935 Novel bro
    11   3338      97.5    3426    6   ARC02473              Arc02473 DNA fragm
    12   3338      97.5    3724    4   AEK54940              Aek54940 Human PIK
    13   3338      97.5    3724    5   AER29796              Aer29796 Breast ca
    14   3338      97.5    3724    7   ARV60468              Arv60468 Human PIK
    15   3338      97.5    3724    7   ARW65283              Arw65283 Human PIK
    16   3338      97.5    3724    7   ATM52123              Atm52123 Human PIK
    17   3338      97.5    3724    7   ATS16021              Ats16021 Human pho
    18   3338      97.5    3724    8   AWY98731              Awy98731 Human PIK
    19   3338      97.5    3724    8   AWY98891              Awy98891 Human PIK
    20   3338      97.5    3724    8   AWY98894              Awy98894 Human PIK
    21   3338      97.5    3724    9   AXU25358              Axu25358 Human pho
    22   3338      97.5    3724    9   AYE41305              Aye41305 Human PIK
    23   3279.4    95.8    4326    8   AWY98838              Awy98838 Human PIK
    24   3205.4    93.6    3207    2   ADH68168              Adh68168 DNA encod
    25   3205.4    93.6    3207    4   AEF64785              Aef64785 Human pho
    26   3145      91.9    7923    8   AWO77361              Awo77361 Expressio
    27   3144.6    91.8    3207    7   ARL60529              Arl60529 Human pho
    28   3143      91.8    3207    4   AEK13519              Aek13519 Phosphati
    29   3141.4    91.7    3207    4   AEK13514              Aek13514 Phosphati
    30   3141.4    91.7    3207    4   AEK13515              Aek13515 Phosphati
    31   3137      91.6    3498    1   AAQ57012              Aaq57012 PtdIns 3-
    32   3118.8    91.1    3210    4   AEK13511              Aek13511 Phosphati
    33   3007      87.8    3207    1   AAQ51155              Aaq51155 p110 cDNA
    34   2640.6    77.1    3207    8   AWY98836              Awy98836 Human PIK
    35   2640.6    77.1    3207    8   AWY98892              Awy98892 Human PIK
    36   1686      49.2    8421    2   ACN43202              Acn43202 Human dia
    37   1515.8    44.3    2397    1   AFS82080              Afs82080 Human tra
    38   1183.4    34.6    1792    3   ADR39810              Adr39810 Human kin
    39   699       20.4    2872    8   AWY98893              Awy98893 Human PIK
    40   564       16.5     741    1   AAA02190              Aaa02190 Human col
    41   564       16.5     741    4   AGD33161              Agd33161 Human pol
    42   530       15.5     716    4   AEK18520              Aek18520 Human PIK
    43   459.2     13.4    3213    1   AAC65690              Aac65690 Human PI3
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44     459.2    13.4    3213    1   AAS14366              Aas14366 cDNA enco
45     459.2    13.4    3213    1   ABV78026              Abv78026 Hypoxia-r
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ALIGNMENTS


RESULT 1
AAS14365
ID   AAS14365 standard; cDNA; 3424 BP.
XX
AC   AAS14365;
XX
DT   11-JUN-2007  (revised)
DT   12-MAR-2002  (first entry)
XX
DE   cDNA encoding human p110alpha isoform of PI3-kinase.
XX
KW   Human; phosphatidylinositol 3-kinase; PI3K; p110alpha isoform; LASP-1;
KW   cancer; inflammatory disease; ophthalmic disorder; SH3 domain;
KW   autoimmune disease; inflammatory bowel disease; bacterial pneumonia;
KW   Type I diabetes mellitus; cytostatic; immunosuppressive; ss.
XX
OS   Homo sapiens.
XX
FH   Key              Location/Qualifiers
FT   CDS              13. .3219
FT                    /*tag=  a
FT                    /product= "p110alpha isoform of PI3-kinase"
XX
PN   WO200185986-A2.
XX
PD   15-NOV-2001.
XX
PF   10-MAY-2001; 2001WO-US015065.
XX
PR   10-MAY-2000; 2000US-0203346P.
XX
PA   (ICOS-) ICOS CORP.
XX
PI   Sadhu C;
XX
DR   WPI; 2002-075252/10.
DR   P-PSDB; AAU09687.
DR   PC:NCBI; gi472990.
DR   PC_ENCPRO:NCBI; gi472991.
XX
PT   Identifying a modulator of p110delta polypeptide binding to SH3 domain-
PT   containing polypeptides e.g. LASP-1, comprising allowing the binding
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PT    partners to interact in the presence and absence of a test compound.
XX
PS    Example 1; Page 55-60; 85pp; English.
XX
CC    The present invention relates to identifying a modulator of the
CC    phosphatidylinositol 3-kinase (PI3K; p110delta) enzyme that binds to the
CC    catalytic subunit via a SH3 domain-containing polypeptide such as LASP-1.
CC    Also described are methods of assaying the specific binding affinity of
CC    the PI3-kinase binding partner. Such modulators are useful for the
CC    treatment of diseases characterised by the undesirable or excessive
CC    activity of PI3Kdelta. For example the modulators can be used for
CC    inhibiting the growth or proliferation of cancer cells (e.g. malignant
CC    neoplasms of lymphoid and reticuloendothelial tissues, Hodgkin's
CC    lymphoma, leukaemias), inflammatory diseases (e.g. rheumatoid arthritis),
CC    ophthalmic disorders (e.g. allergic conjunctivitis), autoimmune diseases
CC    (e.g. systematic lupus erythematosus), inflammatory bowel diseases (e.g.
CC    chronic inflammatory bowel disease), inflammatory dermatoses (e.g.
CC    contact dermatitis; central or peripheral nervous system inflammatory
CC    disorders (e.g. meningitis), bacterial pneumonia, and Type I diabetes
CC    mellitus. The present sequence encodes for human p110alpha isoform of
CC    PI3k
CC
CC    Revised record issued on 11-JUN-2007 : Enhanced with precomputed
CC    information from BOND.
XX
SQ    Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 U; 0 Other;

   Query Match               99.9%;   Score 3422.4;   DB 1;   Length 3424;
   Best Local Similarity     99.9%;
   Matches 3423;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           1 AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG 60
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG 60

Qy          61 CCCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC 120
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 CCCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC 120

Qy         121 CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC 180
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC 180

Qy         181 CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA 240
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA 240

Qy         241 GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAA 300
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    241  GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAA  300

Qy    301  CCATTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAGATCCTCAATCGAGAA  360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  CCATTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAGATCCTCAATCGAGAA  360

Qy    361  ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA  420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA  420

Qy    421  CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTT  480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTT  480

Qy    481  AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG  540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG  540

Qy    541  CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTA  600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTA  600

Qy    601  ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG  660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG  660

Qy    661  CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT  720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT  720

Qy    721  GAACAATTAAAACTCTGTGTTTTAGAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGA  780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  GAACAATTAAAACTCTGTGTTTTAGAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGA  780

Qy    781  TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT  840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT  840

Qy    841  ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA  900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA  900

Qy    901  CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA  960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA  960

Qy    961  TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA  1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA  1020
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Qy    1021  AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT  1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021  AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT  1080

Qy    1081  CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA  1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081  CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA  1140

Qy    1141  CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATACATTCCTGATCTT  1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141  CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATACATTCCTGATCTT  1200

Qy    1201  CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA  1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201  CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA  1260

Qy    1261  GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA  1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261  GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA  1320

Qy    1321  GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG  1380
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Db    1321  GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG  1380

Qy    1381  AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAG  1440
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Db    1381  AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAG  1440

Qy    1441  TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC  1500
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Db    1441  TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC  1500

Qy    1501  AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA  1560
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Db    1501  AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA  1560

Qy    1561  CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA  1620
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561  CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA  1620

Qy    1621  CGAAATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC  1680
            |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621  CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC  1680

Qy    1681  TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT  1740
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681  TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT  1740
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Qy    1741  AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAGATTGGCCTCCAATCAAACCTGAA  1800
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741  AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAGATTGGCCTCCAATCAAACCTGAA  1800

Qy    1801  CAGGCTATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT  1860
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Db    1801  CAGGCTATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT  1860

Qy    1861  CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA  1920
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861  CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA  1920

Qy    1921  CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA  1980
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921  CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA  1980

Qy    1981  GCATTGACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCAC  2040
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1981  GCATTGACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCAC  2040

Qy    2041  AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG  2100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2041  AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG  2100

Qy    2101  ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACTTAACT  2160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2101  ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACTTAACT  2160

Qy    2161  GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT  2220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2161  GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT  2220

Qy    2221  GAGCAAATGAGGCGACCAGATTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC  2280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2221  GAGCAAATGAGGCGACCAGATTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC  2280

Qy    2281  CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAA  2340
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2281  CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAA  2340

Qy    2341  AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC  2400
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2341  AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC  2400

Qy    2401  AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT  2460
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2401  AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT  2460

Qy    2461  ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT  2520
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Db     2461   ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT   2520

Qy     2521   GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT   2580
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     2521   GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT   2580

Qy     2581   ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA   2640
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     2581   ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA   2640

Qy     2641   CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG   2700
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     2641   CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG   2700

Qy     2701   TTTACACGTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT   2760
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     2701   TTTACACGTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT   2760

Qy     2761   CACAATAGTAACATCATGGTGAAAGACGATGGACAACTGTTTCATATAGATTTTGGACAC   2820
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     2761   CACAATAGTAACATCATGGTGAAAGACGATGGACAACTGTTTCATATAGATTTTGGACAC   2820

Qy     2821   TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG   2880
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     2821   TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG   2880

Qy     2881   ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA   2940
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     2881   ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA   2940

Qy     2941   TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT   3000
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     2941   TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT   3000

Qy     3001   CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT   3060
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     3001   CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT   3060

Qy     3061   GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG   3120
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     3061   GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG   3120

Qy     3121   GAGTATTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT   3180
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     3121   GAGTATTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT   3180

Qy     3181   TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA   3240
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Db      3181  TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA  3240

Qy      3241  GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA  3300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3241  GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA  3300

Qy      3301  TAGGAATTGCACAATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACT  3360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3301  TAGGAATTGCACAATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACT  3360

Qy      3361  ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATTTC  3420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3361  ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATTTC  3420

Qy      3421  AAAA  3424
              ||||
Db      3421  AAAA  3424
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RESULT 2
ABL59523
ID    ABL59523 standard; cDNA; 3424 BP.
XX
AC    ABL59523;
XX
DT    11-JUN-2007  (revised)
DT    16-JUL-2002  (first entry)
XX
DE    Human phosphatidylinositol-3-kinase catalytic alpha cDNA SEQ ID NO:23.
XX
KW    Human; phosphatidylinositol-3-kinase catalytic alpha; enzyme; tumour;
KW    lipid associated gene; lipid metabolism; lipid synthesis;
KW    chromosome 3q26.3; gene; ss.
XX
OS    Homo sapiens.
XX
PN    WO200227028-A1.
XX
PD    04-APR-2002.
XX
PF    27-SEP-2001; 2001WO-US030366.
XX
PR    28-SEP-2000; 2000US-00676052.
XX
PA    (ATAI-) ATAIRGIN TECHNOLOGIES INC.
XX
PI    Skinner MK,  Patton JL,  Chaudhary J;
XX
DR    WPI; 2002-405056/43.

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DR      PC:NCBI; gi472990.
DR      PC_ENCPRO:NCBI; gi472991.
XX
PT      Identifying tumor characteristics in a tissue sample taken from a
PT      patient, involves determining the copy number or expression level of
PT      genes associated with lipid metabolism, synthesis or action.
XX
PS      Example 1; Page 82-83; 113pp; English.
XX
CC      The present invention describes a method for identifying tumour
CC      characteristics, comprising measuring a copy number or expression level
CC      of at least two genes associated with lipid metabolism, synthesis, or
CC      action in cells from a patient tissue sample, and comparing the results
CC      with a copy number or expression level of the genes in a normal cell.
CC      Also described is an array of nucleic acid polymers immobilised on a
CC      solid support, comprising a solid support, at least two different nucleic
CC      acid polymers which are each specific for a different gene associated
CC      with lipid metabolism, synthesis or action, where each nucleic acid
CC      polymer is located at a predetermined position on the solid support, and
CC      the array comprises nucleic acid polymers which are specific for less
CC      than 100 genes other than the selected genes. The method is useful for
CC      determining tumour characteristics in a tissue sample taken from a
CC      patient. The present sequence represents a human lipid-associated gene
CC      related cDNA sequence, which is used in the exemplification of the
CC      present invention
CC
CC      Revised record issued on 11-JUN-2007 : Enhanced with precomputed
CC      information from BOND.
XX
SQ      Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 U; 0 Other;

    Query Match              99.9%;   Score 3422.4;   DB 1;   Length 3424;
    Best Local Similarity    99.9%;
    Matches 3423;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG 60

Qy         61 CCCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC 120

Qy        121 CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC 180

Qy        181 CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    181   CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA  240

Qy    241   GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241   GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAA  300

Qy    301   CCATTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301   CCATTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA  360

Qy    361   ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361   ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA  420

Qy    421   CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421   CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTT  480

Qy    481   AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481   AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG  540

Qy    541   CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTA  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541   CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTA  600

Qy    601   ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601   ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG  660

Qy    661   CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT  720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661   CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT  720

Qy    721   GAACAATTAAAACTCTGTGTTTTAGAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGA  780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721   GAACAATTAAAACTCTGTGTTTTAGAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGA  780

Qy    781   TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT  840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781   TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT  840

Qy    841   ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA  900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841   ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA  900

Qy    901   CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA  960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901   CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA  960
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Qy    961  TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA 1020

Qy   1021  AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT 1080

Qy   1081  CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA 1140

Qy   1141  CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTT 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141  CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTT 1200

Qy   1201  CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201  CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA 1260

Qy   1261  GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261  GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA 1320

Qy   1321  GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321  GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG 1380

Qy   1381  AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAG 1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381  AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAG 1440

Qy   1441  TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC 1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441  TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC 1500

Qy   1501  AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA 1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501  AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA 1560

Qy   1561  CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA 1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561  CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA 1620

Qy   1621  CGAAATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC 1680
           |||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621  CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC 1680
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Qy      1681  TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT  1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1681  TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT  1740


Qy      1741  AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAGATTGGCCTCCAATCAAACCTGAA  1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1741  AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAGATTGGCCTCCAATCAAACCTGAA  1800


Qy      1801  CAGGCTATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT  1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1801  CAGGCTATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT  1860


Qy      1861  CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA  1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1861  CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA  1920


Qy      1921  CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA  1980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1921  CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA  1980


Qy      1981  GCATTGACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCAC  2040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1981  GCATTGACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCAC  2040


Qy      2041  AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG  2100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2041  AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG  2100


Qy      2101  ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACTTAACT  2160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2101  ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACTTAACT  2160


Qy      2161  GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAGGTACAGATGAAGTTTTTAGTT  2220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2161  GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAGGTACAGATGAAGTTTTTAGTT  2220


Qy      2221  GAGCAAATGAGGCGACCAGATTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC  2280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2221  GAGCAAATGAGGCGACCAGATTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC  2280


Qy      2281  CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAA  2340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2281  CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAA  2340


Qy      2341  AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC  2400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2341  AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC  2400


Qy      2401  AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT  2460
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           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401  AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT 2460

Qy   2461  ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT 2520
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461  ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT 2520

Qy   2521  GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT 2580
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521  GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT 2580

Qy   2581  ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA 2640
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581  ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA 2640

Qy   2641  CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG 2700
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641  CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG 2700

Qy   2701  TTTACACGTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT 2760
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701  TTTACACGTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT 2760

Qy   2761  CACAATAGTAACATCATGGTGAAAGACGATGGACAACTGTTTCATATAGATTTTGGACAC 2820
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761  CACAATAGTAACATCATGGTGAAAGACGATGGACAACTGTTTCATATAGATTTTGGACAC 2820

Qy   2821  TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG 2880
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821  TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG 2880

Qy   2881  ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA 2940
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881  ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA 2940

Qy   2941  TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT 3000
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941  TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT 3000

Qy   3001  CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT 3060
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001  CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT 3060

Qy   3061  GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG 3120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061  GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG 3120

Qy   3121  GAGTATTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT 3180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db     3121 GAGTATTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAATGGAT 3180

Qy     3181 TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAATGAAA 3240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3181 TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAATGAAA 3240

Qy     3241 GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA 3300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3241 GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA 3300

Qy     3301 TAGGAATTGCACAATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACT 3360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3301 TAGGAATTGCACAATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACT 3360

Qy     3361 ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATTTC 3420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3361 ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATTTC 3420

Qy     3421 AAAA 3424
            ||||
Db     3421 AAAA 3424
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RESULT 3
ADE85076
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ID    ADE85076 standard; DNA; 3424 BP.
XX
AC    ADE85076;
XX
DT    11-JUN-2007  (revised)
DT    29-JAN-2004  (first entry)
XX
DE    Farnesyl transferase inhibitor modulated leukemia associated gene #295.
XX
KW    ss; cytostatic; farnesyl transferase inhibitor; gene expression;
KW    quinolinone; leukemia; cancer.
XX
OS    Homo sapiens.
XX
PN    WO2003038129-A2.
XX
PD    08-MAY-2003.
XX
PF    30-OCT-2002; 2002WO-US034784.
XX
PR    30-OCT-2001; 2001US-0338997P.
PR    30-OCT-2001; 2001US-0340081P.
PR    30-OCT-2001; 2001US-0340938P.
PR    30-OCT-2001; 2001US-0341012P.
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XX
PA    (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
XX
PI    Raponi M;
XX
DR    WPI; 2003-513497/48.
DR    PC:NCBI; gi472990.
DR    PC_ENCPRO:NCBI; gi472991.
XX
PT    Determining whether a patient will respond to treatment with a farnesyl
PT    transferase inhibitor, by analyzing the expression of gene that is
PT    differentially modulated in the presence of the inhibitor.
XX
PS    Disclosure; SEQ ID NO 295; 346pp; English.
XX
CC    The invention relates to a method of determining whether a patient will
CC    respond to treatment with a farnesyl transferase inhibitor (FTI), by
CC    analyzing the expression of gene that is differentially modulated in the
CC    presence of an FTI. The method is useful for determining whether a
CC    patient will respond to treatment with a FTI such as (B)-6-[amino(4-
CC    chlorophenyl)(1-methyl-1H-imidazol-5-yl)methyl]-4-(3-chlorophenyl)-1-
CC    methyl-2-(1H)quinolinone, monitoring the therapy of a patient, treating a
CC    patient with leukemia with FTI if the analysis indicates that the patient
CC    will respond. This sequence corresponds to a gene whose expression may be
CC    modulated in the presence of FTI.
CC
CC    Revised record issued on 11-JUN-2007 : Enhanced with precomputed
CC    information from BOND.
XX
SQ    Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 U; 0 Other;

   Query Match                99.9%;   Score 3422.4;  DB 2;  Length 3424;
   Best Local Similarity   99.9%;
   Matches 3423;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         1 AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG 60
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG 60

Qy        61 CCCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC 120
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 CCCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC 120

Qy       121 CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC 180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC 180

Qy       181 CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA 240
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       181 CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA 240


Qy       241 GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAA 300
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAA 300


Qy       301 CCATTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA 360
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 CCATTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA 360


Qy       361 ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA 420
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA 420


Qy       421 CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTT 480
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTT 480


Qy       481 AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG 540
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG 540


Qy       541 CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTA 600
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTA 600


Qy       601 ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG 660
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG 660


Qy       661 CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT 720
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT 720


Qy       721 GAACAATTAAAACTCTGTGTTTTAGAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGA 780
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 GAACAATTAAAACTCTGTGTTTTAGAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGA 780


Qy       781 TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT 840
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT 840


Qy       841 ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA 900
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA 900


Qy       901 CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA 960
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA 960
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Qy    961  TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA  1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA  1020

Qy   1021  AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT  1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT  1080

Qy   1081  CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA  1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA  1140

Qy   1141  CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTT  1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141  CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTT  1200

Qy   1201  CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA  1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201  CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA  1260

Qy   1261  GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA  1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261  GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA  1320

Qy   1321  GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG  1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321  GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG  1380

Qy   1381  AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAG  1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381  AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAG  1440

Qy   1441  TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC  1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441  TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC  1500

Qy   1501  AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA  1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501  AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA  1560

Qy   1561  CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA  1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561  CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA  1620

Qy   1621  CGAAATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC  1680
           |||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621  CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC  1680
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Qy   1681 TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT 1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT 1740

Qy   1741 AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAGATTGGCCTCCAATCAAACCTGAA 1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAGATTGGCCTCCAATCAAACCTGAA 1800

Qy   1801 CAGGCTATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT 1860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 CAGGCTATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT 1860

Qy   1861 CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA 1920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA 1920

Qy   1921 CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA 1980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA 1980

Qy   1981 GCATTGACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCAC 2040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 GCATTGACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCAC 2040

Qy   2041 AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG 2100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG 2100

Qy   2101 ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACTTAACT 2160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACTTAACT 2160

Qy   2161 GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT 2220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT 2220

Qy   2221 GAGCAAATGAGGCGACCAGATTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC 2280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 GAGCAAATGAGGCGACCAGATTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC 2280

Qy   2281 CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAA 2340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAA 2340

Qy   2341 AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC 2400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC 2400

Qy   2401 AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT 2460
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            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401   AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT   2460


Qy   2461   ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT   2520
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461   ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT   2520


Qy   2521   GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT   2580
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521   GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT   2580


Qy   2581   ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA   2640
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581   ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA   2640


Qy   2641   CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG   2700
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641   CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG   2700


Qy   2701   TTTACACGTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT   2760
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701   TTTACACGTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT   2760


Qy   2761   CACAATAGTAACATCATGGTGAAAGACGATGGACAACTGTTTCATATAGATTTTGGACAC   2820
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761   CACAATAGTAACATCATGGTGAAAGACGATGGACAACTGTTTCATATAGATTTTGGACAC   2820


Qy   2821   TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG   2880
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821   TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG   2880


Qy   2881   ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA   2940
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881   ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA   2940


Qy   2941   TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT   3000
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941   TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT   3000


Qy   3001   CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT   3060
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001   CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT   3060


Qy   3061   GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG   3120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061   GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG   3120


Qy   3121   GAGTATTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT   3180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db     3121 GAGTATTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAATGGAT 3180

Qy     3181 TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA 3240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3181 TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA 3240

Qy     3241 GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA 3300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3241 GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA 3300

Qy     3301 TAGGAATTGCACAATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACT 3360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3301 TAGGAATTGCACAATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACT 3360

Qy     3361 ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATTTC 3420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3361 ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATTTC 3420

Qy     3421 AAAA 3424
            ||||
Db     3421 AAAA 3424
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RESULT 4
ADZ00490
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ID    ADZ00490 standard; cDNA; 3424 BP.
XX
AC    ADZ00490;
XX
DT    11-JUN-2007  (revised)
DT    16-JUN-2005  (first entry)
XX
DE    p110-beta coding sequence.
XX
KW    ss; Anorectic; Antidiabetic; p110-beta; phosphoinositide 3-kinase; p85;
KW    ras; insulin resistance; obesity; gene.
XX
OS    Homo sapiens.
XX
FH    Key             Location/Qualifiers
FT    CDS             13. .3219
FT                    /*tag=  a
XX
PN    WO2005031341-A2.
XX
PD    07-APR-2005.
XX
PF    28-SEP-2004; 2004WO-IB003926.
XX
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PR     29-SEP-2003; 2003US-0507226P.
PR     13-JUL-2004; 2004US-0587333P.
XX
PA     (PFIZ ) PFIZER HEALTH AB.
XX
PI     Bougneres P;
XX
DR     WPI; 2005-273421/28.
DR     P-PSDB; ADZ00491.
DR     GENBANK; Z29090.
DR     PC:NCBI; gi472990.
DR     PC_ENCPRO:NCBI; gi472991.
XX
PT     Predicting a subject's likelihood of developing insulin resistance,
PT     useful for treating insulin resistance and obesity, comprises determining
PT     in a subject the identity of an allele at position 100 of a specific
PT     sequence.
XX
PS     Disclosure; SEQ ID NO 2; 88pp; English.
XX
CC     This sequence represents the p110-beta gene. p110-beta is a catalytic
CC     subunit of a phosphoinositide 3-kinase, which also comprises a regulatory
CC     subunit of about 85 kD. The p110 protein comprises a kinase domain at the
CC     C-terminus, and a p85 and ras binding domain at the N-terminus. The
CC     method of the invention for predicting a subject's likelihood of
CC     developing insulin resistance comprises determining in a subject the
CC     identity of the nucleotide present at a position corresponding to
CC     position -359 of the p110-beta gene , where the allele comprising the
CC     nucleotide is correlated with an increased or decreased likelihood of
CC     developing insulin resistance. The method of the invention is useful for
CC     treating obesity and insulin resistance and for assessing and conducting
CC     clinical trials of medicaments.
CC
CC     Revised record issued on 11-JUN-2007 : Enhanced with precomputed
CC     information from BOND.
XX
SQ     Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 U; 0 Other;

   Query Match              99.9%;   Score 3422.4;   DB 4;   Length 3424;
   Best Local Similarity    99.9%;
   Matches 3423;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        1 AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG 60

Qy       61 CCCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 CCCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC 120
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Qy   121  CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC  180

Qy   181  CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA  240

Qy   241  GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAA  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAA  300

Qy   301  CCATTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAGATCCTCAATCGAGAA  360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  CCATTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAGATCCTCAATCGAGAA  360

Qy   361  ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA  420

Qy   421  CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTT  480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTT  480

Qy   481  AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG  540

Qy   541  CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTA  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTA  600

Qy   601  ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG  660

Qy   661  CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT  720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT  720

Qy   721  GAACAATTAAAACTCTGTGTTTTAGAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGA  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  GAACAATTAAAACTCTGTGTTTTAGAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGA  780

Qy   781  TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT  840
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Qy    841  ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA  900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA  900

Qy    901  CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA  960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA  960

Qy    961  TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA  1020
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA  1020

Qy   1021  AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT  1080
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT  1080

Qy   1081  CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA  1140
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA  1140

Qy   1141  CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTT  1200
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141  CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTT  1200

Qy   1201  CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA  1260
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201  CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA  1260

Qy   1261  GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA  1320
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261  GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA  1320

Qy   1321  GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG  1380
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321  GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG  1380

Qy   1381  AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAG  1440
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381  AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAG  1440

Qy   1441  TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC  1500
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441  TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC  1500

Qy   1501  AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA  1560
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501  AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA  1560

Qy   1561  CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA  1620
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             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1561   CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAGAACAGCTCAAAGCAATTTCTACA   1620

Qy    1621   CGAAATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC   1680
             | | | |   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1621   CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC   1680

Qy    1681   TATTGTGTAACTATCCCCGAATTCTACCCAATTGCTTCTGTCTGTTAAATGGAATTCT   1740
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1681   TATTGTGTAACTATCCCCGAATTCTACCCAATTGCTTCTGTCTGTTAAATGGAATTCT   1740

Qy    1741   AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAGATTGGCCTCCAATCAAACCTGAA   1800
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1741   AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAGATTGGCCTCCAATCAAACCTGAA   1800

Qy    1801   CAGGCTATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT   1860
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1801   CAGGCTATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT   1860

Qy    1861   CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA   1920
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1861   CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA   1920

Qy    1921   CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA   1980
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1921   CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA   1980

Qy    1981   GCATTGACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCAC   2040
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1981   GCATTGACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCAC   2040

Qy    2041   AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG   2100
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    2041   AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG   2100

Qy    2101   ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACTTAACT   2160
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    2101   ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACTTAACT   2160

Qy    2161   GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT   2220
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    2161   GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT   2220

Qy    2221   GAGCAAATGAGGCGACCAGATTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC   2280
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    2221   GAGCAAATGAGGCGACCAGATTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC   2280

Qy    2281   CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAA   2340
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Db    2281  CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAA  2340

Qy    2341  AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC  2400
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2341  AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC  2400

Qy    2401  AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT  2460
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2401  AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT  2460

Qy    2461  ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT  2520
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2461  ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT  2520

Qy    2521  GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT  2580
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2521  GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT  2580

Qy    2581  ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA  2640
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2581  ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA  2640

Qy    2641  CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG  2700
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2641  CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG  2700

Qy    2701  TTTACACGTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT  2760
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2701  TTTACACGTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT  2760

Qy    2761  CACAATAGTAACATCATGGTGAAAGACGATGGACAACTGTTTCATATAGATTTTGGACAC  2820
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2761  CACAATAGTAACATCATGGTGAAAGACGATGGACAACTGTTTCATATAGATTTTGGACAC  2820

Qy    2821  TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG  2880
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2821  TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG  2880

Qy    2881  ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA  2940
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2881  ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA  2940

Qy    2941  TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT  3000
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2941  TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT  3000

Qy    3001  CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT  3060
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3001  CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT  3060
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Qy      3061  GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG  3120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3061  GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG  3120

Qy      3121  GAGTATTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT  3180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3121  GAGTATTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT  3180

Qy      3181  TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA  3240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3181  TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA  3240

Qy      3241  GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA  3300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3241  GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA  3300

Qy      3301  TAGGAATTGCACAATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACT  3360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3301  TAGGAATTGCACAATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACT  3360

Qy      3361  ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATTTC  3420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3361  ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATTTC  3420

Qy      3421  AAAA  3424
              ||||
Db      3421  AAAA  3424
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RESULT 5
AEH10445
ID    AEH10445 standard; cDNA; 3424 BP.
XX
AC    AEH10445;
XX
DT    11-JUN-2007   (revised)
DT    01-JUN-2006   (first entry)
XX
DE    PIK3CA cDNA SEQ ID 831.
XX
KW    gene expression; prognosis; diagnosis; DNA microarray;
KW    colorectal disease; colon tumor; colorectal tumor; cytostatic;
KW    gastrointestinal disease; neoplasm; ss.
XX
OS    Unidentified.
XX
PN    WO2005054508-A2.
XX
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PD     16-JUN-2005.
XX
PF     01-DEC-2004; 2004WO-IB004323.
XX
PR     01-DEC-2003; 2003US-0525987P.
PR     01-DEC-2004; 2004US-00000688.
XX
PA     (IPSO-) IPSOGEN.
PA     (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA     (PAOL-) INST PAOLI CALMETTES IPC.
XX
PI     Bertucci F,  Houlgatte R,  Birnbaum D,  Debono S;
XX
DR     WPI; 2005-435408/44.
DR     PC:NCBI; gi472990.
XX
PT     Analyzing differential gene expression associated with histopathologic
PT     features of colorectal disease, involves detecting overexpression or
PT     underexpression of pool of polynucleotide sequences in colon tissues.
XX
PS     Claim 1; SEQ ID NO 831; 154pp; English.
XX
CC     The invention describes a method of analyzing (M1) differential gene
CC     expression associated with histopathologic features of colorectal
CC     disease, comprising detecting overexpression or underexpression of a pool
CC     of polynucleotide sequences in colon tissues, the pool selected in each
CC     of predefined polynucleotide sequence sets chosen from any one of 644
CC     sequence sets comprising combinations of SEQ ID No. 1-1596, fully defined
CC     in the specification. Also described are: a polynucleotide library (I)
CC     useful for the molecular characterization of a colon cancer, comprising
CC     or corresponding to a pool of polynucleotide sequences either
CC     overexpressed or underexpressed in colon tissue, the pool corresponding
CC     to all or part of the polynucleotide sequence chosen from PS1; and
CC     assigning (M2) a therapeutic regimen to patient with histopathological
CC     features of colorectal disease, e.g. colon cancer, comprising classifying
CC     the patient having a poor prognosis or a good prognosis on the basis of
CC     (M1), assigning the patient a therapeutic regimen, the therapeutic
CC     regiment comprising no adjuvant chemotherapy if the patient is lymph node
CC     negative and is classified as having a good prognosis or comprising
CC     chemotherapy if the patient has any other combination of lymph node
CC     status and expression profile. (M1) is useful for analyzing differential
CC     gene expression associated with histopathologic features of colorectal
CC     disease. (M1) is useful for analyzing differential gene expression
CC     associated with colon tumors, visceral metastases in colon cancer, lymph
CC     node metastases in colon cancer, MSI phenotype in colon cancer, location
CC     of primary colorectal carcinoma, in colon cancer, and survival and death
CC     of patient in colon cancer, where the analysis comprises detection of
CC     overexpression or underexpression of pool of polynucleotide sequences in
CC     colon tissue, the pool corresponding to specific combination of
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CC    polynucleotide sequences from PS1, as given in the specification. (M1) is
CC    useful for detecting, diagnosing, staging, classifying, monitoring or
CC    predicting conditions associated with colorectal cancer. (M1) is useful
CC    for prognosis or diagnosis or colon cancer or for monitoring the
CC    treatment of a patient with colon cancer, which involves implementing
CC    (M1) on nucleic acids from the patient. (M1) is useful for
CC    differentiating a normal cell from a cancer cell, which involves
CC    implementing (M1) on nucleic acids from the cells. (M1) is useful for
CC    selecting appropriate doses and/or schedule of chemotherapeutics and/or
CC    (bio)pharmaceuticals and/or target agents e.g. Irinotecan, 5-fluorouracil
CC    and methotrexate. This sequence represents a polynucleotide identified in
CC    the analysis of differential gene expression associated with
CC    histopathological features of colorectal disease. Note: The sequence data
CC    for this patent is not represented in the printed specification but is
CC    based on sequence information supplied by the European Patent Office.
CC
CC    Revised record issued on 11-JUN-2007 : Enhanced with precomputed
CC    information from BOND.
XX
SQ    Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 U; 0 Other;

   Query Match               99.9%;   Score 3422.4;   DB 4;   Length 3424;
   Best Local Similarity   99.9%;
   Matches 3423;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy        1 AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG 60

Qy       61 CCCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 CCCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC 120

Qy      121 CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC 180

Qy      181 CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA 240

Qy      241 GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAA 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAA 300

Qy      301 CCATTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CCATTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA 360
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Qy    361  ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA  420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA  420

Qy    421  CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTT  480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTT  480

Qy    481  AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG  540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG  540

Qy    541  CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTA  600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTA  600

Qy    601  ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG  660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG  660

Qy    661  CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT  720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT  720

Qy    721  GAACAATTAAAACTCTGTGTTTTAGAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGA  780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  GAACAATTAAAACTCTGTGTTTTAGAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGA  780

Qy    781  TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT  840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT  840

Qy    841  ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA  900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA  900

Qy    901  CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA  960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA  960

Qy    961  TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA  1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA  1020

Qy   1021  AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT  1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT  1080

Qy   1081  CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA  1140
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Db   1081  CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA  1140

Qy   1141  CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTT  1200
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   1141  CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTT  1200

Qy   1201  CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA  1260
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   1201  CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA  1260

Qy   1261  GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA  1320
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   1261  GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA  1320

Qy   1321  GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG  1380
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   1321  GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG  1380

Qy   1381  AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAG  1440
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   1381  AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAG  1440

Qy   1441  TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC  1500
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   1441  TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC  1500

Qy   1501  AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA  1560
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   1501  AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA  1560

Qy   1561  CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA  1620
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   1561  CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA  1620

Qy   1621  CGAAATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC  1680
              | | |   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   1621  CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC  1680

Qy   1681  TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT  1740
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   1681  TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT  1740

Qy   1741  AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA  1800
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   1741  AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA  1800

Qy   1801  CAGGCTATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT  1860
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Db    1801  CAGGCTATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT  1860

Qy    1861  CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA  1920
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861  CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA  1920

Qy    1921  CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA  1980
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921  CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA  1980

Qy    1981  GCATTGACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCAC  2040
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1981  GCATTGACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCAC  2040

Qy    2041  AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG  2100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2041  AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG  2100

Qy    2101  ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACTTAACT  2160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2101  ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACTTAACT  2160

Qy    2161  GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAGGTACAGATGAAGTTTTTAGTT  2220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2161  GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAGGTACAGATGAAGTTTTTAGTT  2220

Qy    2221  GAGCAAATGAGGCGACCAGATTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC  2280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2221  GAGCAAATGAGGCGACCAGATTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC  2280

Qy    2281  CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAA  2340
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2281  CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAA  2340

Qy    2341  AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC  2400
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2341  AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC  2400

Qy    2401  AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT  2460
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2401  AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT  2460

Qy    2461  ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT  2520
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2461  ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT  2520

Qy    2521  GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT  2580
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2521  GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT  2580
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Qy    2581  ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA  2640
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2581  ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA  2640

Qy    2641  CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG  2700
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2641  CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG  2700

Qy    2701  TTTACACGTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT  2760
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2701  TTTACACGTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT  2760

Qy    2761  CACAATAGTAACATCATGGTGAAAGACGATGGACAACTGTTTCATATAGATTTTGGACAC  2820
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2761  CACAATAGTAACATCATGGTGAAAGACGATGGACAACTGTTTCATATAGATTTTGGACAC  2820

Qy    2821  TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG  2880
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2821  TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG  2880

Qy    2881  ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA  2940
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2881  ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA  2940

Qy    2941  TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT  3000
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2941  TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT  3000

Qy    3001  CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT  3060
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3001  CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT  3060

Qy    3061  GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG  3120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3061  GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG  3120

Qy    3121  GAGTATTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT  3180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3121  GAGTATTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT  3180

Qy    3181  TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA  3240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3181  TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA  3240

Qy    3241  GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA  3300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3241  GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA  3300
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Qy   3301 TAGGAATTGCACAATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACT 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 TAGGAATTGCACAATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACT 3360


Qy   3361 ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATTTC 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATTTC 3420


Qy   3421 AAAA 3424
          ||||
Db   3421 AAAA 3424
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RESULT 6
AED31618
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ID   AED31618 standard; cDNA; 3424 BP.
XX
AC   AED31618;
XX
DT   15-DEC-2005  (first entry)
XX
DE   cDNA (SEQ ID No:2) encoding human phosphatidylinositol 3-kinase (PIK3CA).
XX
KW   cancer; neoplasm; phosphatidylinositol 3-kinase; PIK3CA; tumor;
KW   chemotherapy; cytostatic; RNA interference; gene silencing;
KW   antisense therapy; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key              Location/Qualifiers
FT   CDS              13. .3219
FT                    /*tag=  a
FT                    /product= "PIK3CA"
XX
PN   WO2005091849-A2.
XX
PD   06-OCT-2005.
XX
PF   18-FEB-2005; 2005WO-US005193.
XX
PR   02-MAR-2004; 2004US-0548886P.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Samuels Y,  Velculescu V,  Kinzler KW,  Vogelstein B;
XX
DR   WPI; 2005-713721/73.
DR   P-PSDB; AED31619.
XX
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PT    Assessing cancer in a human suspected of having cancer, by determining a
PT    non-synonymous, intragenic mutation in a phosphatidylinositol 3-kinase
PT    (PIK3CA) coding sequence in the body sample from a human.
XX
PS    Claim 1; SEQ ID NO 2; 107pp; English.
XX
CC    The invention relates to a method of assessing cancer in a body sample of
CC    a human suspected of having cancer. The method comprises determining a
CC    non-synonymous, intragenic mutation in a phosphatidylinositol 3-kinase
CC    (PIK3CA) coding sequence in the body sample, and identifying the human as
CC    likely to have cancer if a non-synonymous, intragenic mutation in PIK3CA
CC    coding sequence is determined in the body sample. Also described are: (1)
CC    a method of inhibiting progression of a tumor in a human; (2) a method of
CC    identifying candidate chemotherapeutic agents; (3) a method for
CC    delivering an appropriate chemotherapeutic drug to a patient in need; and
CC    (4) a set of one or more primers for amplifying and/or sequencing PIK3CA,
CC    the primers selected from forward primers, reverse primers, or sequencing
CC    primers, where the forward primers are selected from sequences given as
CC    SEQ ID NOs 6-165, the reverse primers are selected from sequences given
CC    as SEQ ID NOs 166-325, and the sequencing primers are selected sequences
CC    given as SEQ ID NOs 326-485 in the specification. The method of the
CC    invention is useful for assessing cancer in a body sample of a human
CC    suspected of having cancer, inhibiting progression of a tumor in a human,
CC    identifying candidate chemotherapeutic agents, and delivering an
CC    appropriate chemotherapeutic drug to a patient in need. This sequence
CC    encodes human PIK3CA.
XX
SQ    Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 U; 0 Other;

   Query Match              99.9%;   Score 3422.4;  DB 4;  Length 3424;
   Best Local Similarity    99.9%;
   Matches 3423;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG 60

Qy         61 CCCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC 120

Qy        121 CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC 180

Qy        181 CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA 240
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Qy      241   GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAA   300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241   GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAA   300

Qy      301   CCATTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA   360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301   CCATTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA   360

Qy      361   ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA   420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361   ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA   420

Qy      421   CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTT   480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421   CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTT   480

Qy      481   AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG   540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481   AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG   540

Qy      541   CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTA   600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541   CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTA   600

Qy      601   ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG   660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601   ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG   660

Qy      661   CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT   720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661   CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT   720

Qy      721   GAACAATTAAAACTCTGTGTTTTAGAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGA   780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721   GAACAATTAAAACTCTGTGTTTTAGAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGA   780

Qy      781   TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT   840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781   TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT   840

Qy      841   ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAGCCTTTATTCTCAA   900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841   ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAGCCTTTATTCTCAA   900

Qy      901   CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA   960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901   CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA   960

Qy      961   TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA   1020
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                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961    TATATGAATGGAGAAACATCTACAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA  1020

Qy      1021    AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT  1080
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021    AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT  1080

Qy      1081    CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA  1140
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081    CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA  1140

Qy      1141    CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTT  1200
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141    CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTT  1200

Qy      1201    CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA  1260
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201    CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA  1260

Qy      1261    GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA  1320
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261    GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA  1320

Qy      1321    GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG  1380
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321    GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG  1380

Qy      1381    AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAG  1440
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381    AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAG  1440

Qy      1441    TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC  1500
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1441    TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC  1500

Qy      1501    AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA  1560
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1501    AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA  1560

Qy      1561    CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA  1620
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1561    CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA  1620

Qy      1621    CGAAATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC  1680
                |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1621    CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC  1680

Qy      1681    TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT  1740
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    1681  TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT  1740

Qy    1741  AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAGATTGGCCTCCAATCAAACCTGAA   1800
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741  AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAGATTGGCCTCCAATCAAACCTGAA   1800

Qy    1801  CAGGCTATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT  1860
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801  CAGGCTATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT  1860

Qy    1861  CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA  1920
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861  CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA  1920

Qy    1921  CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA  1980
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921  CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA  1980

Qy    1981  GCATTGACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCAC  2040
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1981  GCATTGACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCAC  2040

Qy    2041  AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG  2100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2041  AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG  2100

Qy    2101  ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACTTAACT  2160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2101  ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACTTAACT  2160

Qy    2161  GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT  2220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2161  GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT  2220

Qy    2221  GAGCAAATGAGGCGACCAGATTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC  2280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2221  GAGCAAATGAGGCGACCAGATTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC  2280

Qy    2281  CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAA  2340
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2281  CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAA  2340

Qy    2341  AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC  2400
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2341  AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC  2400

Qy    2401  AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT  2460
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2401  AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT  2460
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Qy   2461  ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT  2520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461  ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT  2520

Qy   2521  GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT  2580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521  GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT  2580

Qy   2581  ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA  2640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581  ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA  2640

Qy   2641  CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG  2700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641  CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG  2700

Qy   2701  TTTACACGTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT  2760
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701  TTTACACGTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT  2760

Qy   2761  CACAATAGTAACATCATGGTGAAAGACGATGGACAACTGTTTCATATAGATTTTGGACAC  2820
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761  CACAATAGTAACATCATGGTGAAAGACGATGGACAACTGTTTCATATAGATTTTGGACAC  2820

Qy   2821  TTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG  2880
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821  TTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG  2880

Qy   2881  ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA  2940
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881  ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA  2940

Qy   2941  TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT  3000
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941  TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT  3000

Qy   3001  CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT  3060
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001  CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT  3060

Qy   3061  GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG  3120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061  GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG  3120

Qy   3121  GAGTATTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT  3180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121  GAGTATTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT  3180
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Qy    3181  TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA 3240
            ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db    3181  TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA 3240

Qy    3241  GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA 3300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3241  GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA 3300

Qy    3301  TAGGAATTGCACAATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACT 3360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3301  TAGGAATTGCACAATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACT 3360

Qy    3361  ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATTTC 3420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3361  ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATTTC 3420

Qy    3421  AAAA 3424
            ||||
Db    3421  AAAA 3424
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RESULT 7
AEG93388
ID    AEG93388 standard; cDNA; 3424 BP.
XX
AC    AEG93388;
XX
DT    11-JUN-2007  (revised)
DT    01-JUN-2006  (first entry)
XX
DE    Human tumor cell cDNA SEQ ID NO:884.
XX
KW    Gene expression; tumor; ss.
XX
OS    Homo sapiens.
XX
PN    WO2006036025-A1.
XX
PD    06-APR-2006.
XX
PF    30-SEP-2005; 2005WO-JP018574.
XX
PR    30-SEP-2004; 2004JP-00286259.
PR    28-FEB-2005; 2005JP-00054475.
PR    28-FEB-2005; 2005JP-00054866.
XX
PA    (EISA ) EISAI CO LTD.
XX
PI    Owa T,  Yokoi A,  Ozawa Y,  Kawai T,  Ushijima R;

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XX
DR    WPI; 2006-293404/30.
DR    PC:NCBI; gi472990.
DR    PC_ENCPRO:NCBI; gi472991.
XX
PT    Evaluating sensitivity of a tumor cell to a sulfonamide-containing
PT    compound, comprises comparing the expression of specific genes in tumor
PT    cells before and after administration of the compound.
XX
PS    Claim 1; SEQ ID NO 884; 1405pp; Japanese.
XX
CC    The invention relates to a method of evaluating the sensitivity of a
CC    tumor cell to a sulfonamide-containing compound, by comparing the
CC    expression level of genes in tumor cells obtained from cancer patients
CC    before and after administration of the sulfonamide-containing compound
CC    and determining the tumor cell to be sensitive to the sulfonamide-
CC    containing compound, when the expression amount of genes in the cell is
CC    increased compared with the expression amount before administration
CC    and/or when the expression amount of one or more genes is decreased
CC    compared with the expression amount before administration. The invention
CC    also relates to an assay reagent of RNA comprising an oligonucleotide
CC    complementary to an RNA which is the transcription product of a gene, and
CC    an immunoassay reagent containing the antibody with respect to a protein
CC    which is a translation product of the gene. The expression level of the
CC    gene, which is the RNA transcription product, is measured using a DNA
CC    microarray or by quantitative PCR. The expression level of protein, which
CC    is a translation product of the gene, is measured by an immunochemical
CC    method such as enzyme linked immunosorbent assay (ELISA),
CC    radioimmunoassay (RIA) or Western blotting. The method enables evaluation
CC    of the sensitivity of a tumor cell to a sulfonamide-containing compound.
CC    This sequence represents human tumor cell cDNA used in the scope of the
CC    invention.
CC
CC    Revised record issued on 11-JUN-2007 : Enhanced with precomputed
CC    information from BOND.
XX
SQ    Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 U; 0 Other;

    Query Match                99.9%;   Score 3422.4;   DB 4;   Length 3424;
    Best Local Similarity   99.9%;
    Matches 3423;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy      1 AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG 60

Qy     61 CCCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CCCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC 120
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Qy   121  CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC  180

Qy   181  CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA  240

Qy   241  GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAA  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAA  300

Qy   301  CCATTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAGATCCTCAATCGAGAA  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  CCATTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAGATCCTCAATCGAGAA  360

Qy   361  ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA  420

Qy   421  CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTT  480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTT  480

Qy   481  AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG  540

Qy   541  CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTA  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTA  600

Qy   601  ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG  660

Qy   661  CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT  720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT  720

Qy   721  GAACAATTAAAACTCTGTGTTTTAGAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGA  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  GAACAATTAAAACTCTGTGTTTTAGAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGA  780

Qy   781  TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT  840
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Qy        841 ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA 900
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA 900

Qy        901 CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA 960
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA 960

Qy        961 TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA 1020
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA 1020

Qy       1021 AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT 1080
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT 1080

Qy       1081 CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA 1140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA 1140

Qy       1141 CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATACATTCCTGATCTT 1200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATACATTCCTGATCTT 1200

Qy       1201 CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA 1260
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA 1260

Qy       1261 GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA 1320
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA 1320

Qy       1321 GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG 1380
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG 1380

Qy       1381 AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAG 1440
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAG 1440

Qy       1441 TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC 1500
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC 1500

Qy       1501 AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA 1560
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA 1560

Qy       1561 CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA 1620
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                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1561   CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA  1620

Qy      1621   CGAAATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC  1680
                   |||  |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1621   CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC  1680

Qy      1681   TATTGTGTAACTATCCCCGAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT  1740
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1681   TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT  1740

Qy      1741   AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAGATTGGCCTCCAATCAAACCTGAA  1800
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1741   AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAGATTGGCCTCCAATCAAACCTGAA  1800

Qy      1801   CAGGCTATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT  1860
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1801   CAGGCTATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT  1860

Qy      1861   CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA  1920
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1861   CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA  1920

Qy      1921   CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA  1980
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1921   CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA  1980

Qy      1981   GCATTGACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCAC  2040
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1981   GCATTGACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCAC  2040

Qy      2041   AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG  2100
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2041   AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG  2100

Qy      2101   ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACTTAACT  2160
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2101   ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACTTAACT  2160

Qy      2161   GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT  2220
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2161   GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT  2220

Qy      2221   GAGCAAATGAGGCGACCAGATTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC  2280
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2221   GAGCAAATGAGGCGACCAGATTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC  2280

Qy      2281   CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAA  2340
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   2281  CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAA  2340

Qy   2341  AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC  2400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341  AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC  2400

Qy   2401  AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT  2460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401  AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT  2460

Qy   2461  ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT  2520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461  ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT  2520

Qy   2521  GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT  2580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521  GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT  2580

Qy   2581  ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA  2640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581  ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA  2640

Qy   2641  CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG  2700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641  CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG  2700

Qy   2701  TTTACACGTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT  2760
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701  TTTACACGTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT  2760

Qy   2761  CACAATAGTAACATCATGGTGAAAGACGATGGACAACTGTTTCATATAGATTTTGGACAC  2820
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761  CACAATAGTAACATCATGGTGAAAGACGATGGACAACTGTTTCATATAGATTTTGGACAC  2820

Qy   2821  TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG  2880
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821  TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG  2880

Qy   2881  ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA  2940
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881  ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA  2940

Qy   2941  TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT  3000
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941  TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT  3000

Qy   3001  CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT  3060
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001  CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT  3060
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Qy      3061  GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG 3120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3061  GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG 3120

Qy      3121  GAGTATTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT 3180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3121  GAGTATTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT 3180

Qy      3181  TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA 3240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3181  TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA 3240

Qy      3241  GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA 3300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3241  GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA 3300

Qy      3301  TAGGAATTGCACAATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACT 3360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3301  TAGGAATTGCACAATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACT 3360

Qy      3361  ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATTTC 3420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3361  ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATTTC 3420

Qy      3421  AAAA 3424
              ||||
Db      3421  AAAA 3424
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RESULT 8
AAQ51156

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ID    AAQ51156 standard; cDNA; 3412 BP.
XX
AC    AAQ51156;
XX
DT    25-MAR-2003  (revised)
DT    12-APR-1994  (first entry)
XX
DE    Human p110 cDNA.
XX
KW    Phosphoinositide kinase; PI; p85 subunit; screening; agonist; antagonist;
KW    cell proliferation; inhibition; prophylaxis; therapy; platelets;
KW    neutorphil activity; 3-phosphorylated phosphoinositides; ds.
XX
OS    Homo sapiens.
XX
FH    Key            Location/Qualifiers
FT    CDS            1. .3207
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FT                          /*tag=  a
FT                          /note= "PI3- kinase p110"
XX
PN    WO9321328-A1.
XX
PD    28-OCT-1993.
XX
PF    13-APR-1993;    93WO-GB000761.
XX
PR    13-APR-1992;    92GB-00008135.
XX
PA    (LUDW-) LUDWIG INST CANCER RES.
XX
PI    Hiles ID,  Fry MJ,  Dhand R,  Waterfield MD,  Parker PJ,  Otsu M;
PI    Panayotou G,  Volinia S,  Gout I;
XX
DR    WPI; 1993-351738/44.
DR    P-PSDB; AAR43342.
XX
PT    Recombinant polypeptide(s) - with phosphoinositide-3 kinase activity,
PT    useful for controlling cell proliferation.
XX
PS    Claim 7; Fig 16; 146pp; English.
XX
CC    Southern blot analysis was performed using a bovine cDNA probe contg. a
CC    fragment of a PI3-kinase-encoding sequence and human cDNA isolated from a
CC    cDNA library constructed from mRNA isolated from the human cell line
CC    KG1a. Positive clones were sequenced to give the human PI3 kinase p110
CC    sequence shown. This sequence has 95 percent homology with the bovine
CC    sequence. The domain encoding residues 19- 100 of human p110 is
CC    sufficient to encode the kinase which will associate with the p85 kinase
CC    subunit. The gene may be used to provide a protein with PI3 kinase
CC    activity, and is useful for screening for (ant)agonists of PI3 kinase
CC    activity which could be useful for stimulation or inhibition of cell
CC    proliferation and hence prophylaxis or therapy. Platelet or neutrophil
CC    activity or blood glucose levels can be controlled using the kinase. See
CC    also AAQ51155 and AAQ57522-3. (Updated on 25-MAR-2003 to correct PN
CC    field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ    Sequence 3412 BP; 1128 A; 616 C; 706 G; 962 T; 0 U; 0 Other;

   Query Match                 99.6%;   Score 3410.4;   DB 1;   Length 3412;
   Best Local Similarity    99.9%;
   Matches 3411;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        13 ATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATGCCCCCAAGAATC 72
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 ATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATGCCCCCAAGAATC 60
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Qy        73  CTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGCCTCCGTGAGGCT 132
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61  CTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGCCTCCGTGAGGCT 120

Qy       133  ACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATACCCTCTCCATCAA 192
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121  ACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATACCCTCTCCATCAA 180

Qy       193  CTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAAGCAGAAAGGGAA 252
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181  CTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAAGCAGAAAGGGAA 240

Qy       253  GAATTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAACCATTTTTAAAA 312
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241  GAATTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAACCATTTTTAAAA 300

Qy       313  GTAATTGAACCAGTAGGCAACCGTGAAGAAAGATCCTCAATCGAGAAATTGGTTTTGCT 372
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301  GTAATTGAACCAGTAGGCAACCGTGAAGAAAGATCCTCAATCGAGAAATTGGTTTTGCT 360

Qy       373  ATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTACAGGACTTCCGA 432
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361  ATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTACAGGACTTCCGA 420

Qy       433  AGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTTAATTCACCTCAT 492
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421  AGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTTAATTCACCTCAT 480

Qy       493  AGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAGCTGCCAAAGCAC 552
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481  AGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAGCTGCCAAAGCAC 540

Qy       553  ATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTAATAGTTTCTCCA 612
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541  ATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTAATAGTTTCTCCA 600

Qy       613  AATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTGCCAGAACAAGTA 672
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601  AATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTGCCAGAACAAGTA 660

Qy       673  ATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCTGAACAATTAAAA 732
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661  ATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCTGAACAATTAAAA 720

Qy       733  CTCTGTGTTTTAGAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGATGTGATGAATAC 792
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721  CTCTGTGTTTTAGAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGATGTGATGAATAC 780

Qy       793  TTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGTATAATGCTTGGG 852
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  TTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGTATAATGCTTGGG  840

Qy    853  AGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAACTGCCAATGGAC  912
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  AGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAACTGCCAATGGAC  900

Qy    913  TGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCATATATGAATGGA  972
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  TGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCATATATGAATGGA  960

Qy    973  GAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATAAAAATTCTTTGT  1032
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  GAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATAAAAATTCTTTGT  1020

Qy   1033  GCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTTCGAACAGGTATC  1092
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  GCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTTCGAACAGGTATC  1080

Qy   1093  TACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTACCTTGTTCCAAT  1152
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  TACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTACCTTGTTCCAAT  1140

Qy   1153  CCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTTCCTCGTGCTGCT  1212
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141  CCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTTCCTCGTGCTGCT  1200

Qy   1213  CGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAAGAGGAACACTGT  1272
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201  CGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAAGAGGAACACTGT  1260

Qy   1273  CCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTAGTATCTGGAAAA  1332
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261  CCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTAGTATCTGGAAAA  1320

Qy   1333  ATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTGAACCCTATTGGT  1392
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321  ATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTGAACCCTATTGGT  1380

Qy   1393  GTTACTGGATCAAATCCAAATAAAGAACTCCATGCTTAGAGTTGGAGTTTGACTGGTTC  1452
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381  GTTACTGGATCAAATCCAAATAAAGAACTCCATGCTTAGAGTTGGAGTTTGACTGGTTC  1440

Qy   1453  AGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCCAATTGGTCTGTA  1512
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441  AGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCCAATTGGTCTGTA  1500

Qy   1513  TCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGACTAGCTAGAGAC  1572
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    1501  TCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGACTAGCTAGAGAC  1560

Qy    1573  AATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAAATCCTCTC  1632
            |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db    1561  AATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAGATCCTCTC  1620

Qy    1633  TCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGTGTAACT  1692
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621  TCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGTGTAACT  1680

Qy    1693  ATCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCTAGAGATGAAGTA  1752
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681  ATCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCTAGAGATGAAGTA  1740

Qy    1753  GCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCTATGGAA  1812
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741  GCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCTATGGAA  1800

Qy    1813  CTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCGGTGCTTGGAA  1872
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801  CTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCGGTGCTTGGAA  1860

Qy    1873  AAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGGTCCTAAAA  1932
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861  AAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGGTCCTAAAA  1920

Qy    1933  TATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAAGCATTGACTAAT  1992
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921  TATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAAGCATTGACTAAT  1980

Qy    1993  CAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCACAATAAAACAGTT  2052
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1981  CAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCACAATAAAACAGTT  2040

Qy    2053  AGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGGATGTATTTGAAG  2112
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2041  AGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGGATGTATTTGAAG  2100

Qy    2113  CACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACTTAACTGACATTCTCAAA  2172
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2101  CACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACTTAACTGACATTCTCAAA  2160

Qy    2173  CAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTTGAGCAAATGAGG  2232
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2161  CAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTTGAGCAAATGAGG  2220

Qy    2233  CGACCAGATTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAACCCTGCTCATCAA  2292
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2221  CGACCAGATTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAACCCTGCTCATCAA  2280
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Qy   2293  CTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAAAGGCCACTGTGG  2352
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281  CTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAAAGGCCACTGTGG  2340

Qy   2353  TTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAACAATGAGATCATC  2412
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341  TTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAACAATGAGATCATC  2400

Qy   2413  TTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATTATTCGTATTATG  2472
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401  TTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATTATTCGTATTATG  2460

Qy   2473  GAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTATGGTTGTCTGTCA  2532
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461  GAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTATGGTTGTCTGTCA  2520

Qy   2533  ATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACTATTATGCAAATT  2592
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521  ATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACTATTATGCAAATT  2580

Qy   2593  CAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACTACATCAGTGG  2652
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581  CAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACTACATCAGTGG  2640

Qy   2653  CTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTGTTTACACGTTCA  2712
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641  CTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTGTTTACACGTTCA  2700

Qy   2713  TGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGTCACAATAGTAAC  2772
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701  TGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGTCACAATAGTAAC  2760

Qy   2773  ATCATGGTGAAAGACGATGGACAACTGTTTCATATAGATTTTGGACACTTTTTGGATCAC  2832
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761  ATCATGGTGAAAGACGATGGACAACTGTTTCATATAGATTTTGGACACTTTTTGGATCAC  2820

Qy   2833  AAGAAGAAAAATTTGGTTATAAACGAGAACGTGTGCCATTGTTTTGACACAGGATTTC  2892
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821  AAGAAGAAAAATTTGGTTATAAACGAGAACGTGTGCCATTGTTTTGACACAGGATTTC  2880

Qy   2893  TTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAATTTGAGAGGTTT  2952
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881  TTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAATTTGAGAGGTTT  2940

Qy   2953  CAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAATCTCTTCATAAAT  3012
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941  CAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAATCTCTTCATAAAT  3000
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Qy      3013 CTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTTGATGACATTGCA 3072
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3001 CTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTTGATGACATTGCA 3060

Qy      3073 TACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTGGAGTATTTCATG 3132
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3061 TACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTGGAGTATTTCATG 3120

Qy      3133 AAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGATTGGATCTTCCAC 3192
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3121 AAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGATTGGATCTTCCAC 3180

Qy      3193 ACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAAGCTCACTCTGGA 3252
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3181 ACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAAGCTCACTCTGGA 3240

Qy      3253 TTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCATAGGAATTGCAC 3312
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3241 TTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCATAGGAATTGCAC 3300

Qy      3313 AATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACTATATAATTTAAA 3372
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3301 AATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACTATATAATTTAAA 3360

Qy      3373 TAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATTTCAAAA 3424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3361 TAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATTTCAAAA 3412
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RESULT 9
AED31617
ID    AED31617 standard; cDNA; 3412 BP.
XX
AC    AED31617;
XX
DT    15-DEC-2005   (first entry)
XX
DE    cDNA (SEQ ID No:1) encoding human phosphatidylinositol 3-kinase (PIK3CA).
XX
KW    cancer; neoplasm; phosphatidylinositol 3-kinase; PIK3CA; tumor;
KW    chemotherapy; cytostatic; RNA interference; gene silencing;
KW    antisense therapy; gene; ss.
XX
OS    Homo sapiens.
XX
FH    Key             Location/Qualifiers
FT    CDS             1. .3207
FT                    /*tag=  a
FT                    /product= "PIK3CA"
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XX
PN   WO2005091849-A2.
XX
PD   06-OCT-2005.
XX
PF   18-FEB-2005; 2005WO-US005193.
XX
PR   02-MAR-2004; 2004US-0548886P.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Samuels Y,  Velculescu V,  Kinzler KW,  Vogelstein B;
XX
DR   WPI; 2005-713721/73.
DR   P-PSDB; AED31619.
XX
PT   Assessing cancer in a human suspected of having cancer, by determining a
PT   non-synonymous, intragenic mutation in a phosphatidylinositol 3-kinase
PT   (PIK3CA) coding sequence in the body sample from a human.
XX
PS   Disclosure; SEQ ID NO 1; 107pp; English.
XX
CC   The invention relates to a method of assessing cancer in a body sample of
CC   a human suspected of having cancer. The method comprises determining a
CC   non-synonymous, intragenic mutation in a phosphatidylinositol 3-kinase
CC   (PIK3CA) coding sequence in the body sample, and identifying the human as
CC   likely to have cancer if a non-synonymous, intragenic mutation in PIK3CA
CC   coding sequence is determined in the body sample. Also described are: (1)
CC   a method of inhibiting progression of a tumor in a human; (2) a method of
CC   identifying candidate chemotherapeutic agents; (3) a method for
CC   delivering an appropriate chemotherapeutic drug to a patient in need; and
CC   (4) a set of one or more primers for amplifying and/or sequencing PIK3CA,
CC   the primers selected from forward primers, reverse primers, or sequencing
CC   primers, where the forward primers are selected from sequences given as
CC   SEQ ID NOs 6-165, the reverse primers are selected from sequences given
CC   as SEQ ID NOs 166-325, and the sequencing primers are selected sequences
CC   given as SEQ ID NOs 326-485 in the specification. The method of the
CC   invention is useful for assessing cancer in a body sample of a human
CC   suspected of having cancer, inhibiting progression of a tumor in a human,
CC   identifying candidate chemotherapeutic agents, and delivering an
CC   appropriate chemotherapeutic drug to a patient in need. This sequence
CC   encodes human PIK3CA.
XX
SQ   Sequence 3412 BP; 1128 A; 616 C; 706 G; 962 T; 0 U; 0 Other;

   Query Match              99.6%;   Score 3410.4;   DB 4;   Length 3412;
   Best Local Similarity    99.9%;
   Matches 3411;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy      13 ATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATGCCCCCAAGAATC 72
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATGCCCCCAAGAATC 60

Qy      73 CTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGCCTCCGTGAGGCT 132
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGCCTCCGTGAGGCT 120

Qy     133 ACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATACCCTCTCCATCAA 192
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATACCCTCTCCATCAA 180

Qy     193 CTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAAGCAGAAAGGGAA 252
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAAGCAGAAAGGGAA 240

Qy     253 GAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAACCATTTTTAAAA 312
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAACCATTTTTAAAA 300

Qy     313 GTAATTGAACCAGTAGGCAACCGTGAAGAAAGATCCTCAATCGAGAAATTGGTTTTGCT 372
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 GTAATTGAACCAGTAGGCAACCGTGAAGAAAGATCCTCAATCGAGAAATTGGTTTTGCT 360

Qy     373 ATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTACAGGACTTCCGA 432
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 ATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTACAGGACTTCCGA 420

Qy     433 AGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTTAATTCACCTCAT 492
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 AGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTTAATTCACCTCAT 480

Qy     493 AGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAGCTGCCAAAGCAC 552
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 AGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAGCTGCCAAAGCAC 540

Qy     553 ATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTAATAGTTTCTCCA 612
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 ATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTAATAGTTTCTCCA 600

Qy     613 AATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTGCCAGAACAAGTA 672
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 AATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTGCCAGAACAAGTA 660

Qy     673 ATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCTGAACAATTAAAA 732
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 ATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCTGAACAATTAAAA 720

Qy     733 CTCTGTGTTTTAGAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGATGTGATGAATAC 792
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Db      721   CTCTGTGTTTTAGAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGATGTGATGAATAC 780

Qy      793   TTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGTATAATGCTTGGG 852
                    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      781   TTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGTATAATGCTTGGG 840

Qy      853   AGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAACTGCCAATGGAC 912
                    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      841   AGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAACTGCCAATGGAC 900

Qy      913   TGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCATATATGAATGGA 972
                    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      901   TGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCATATATGAATGGA 960

Qy      973   GAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATAAAAATTCTTTGT 1032
                    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      961   GAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATAAAAATTCTTTGT 1020

Qy      1033  GCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTTCGAACAGGTATC 1092
                    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1021  GCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTTCGAACAGGTATC 1080

Qy      1093  TACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTACCTTGTTCCAAT 1152
                    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1081  TACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTACCTTGTTCCAAT 1140

Qy      1153  CCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTTCCTCGTGCTGCT 1212
                    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1141  CCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTTCCTCGTGCTGCT 1200

Qy      1213  CGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAAGAGGAACACTGT 1272
                    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1201  CGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAAGAGGAACACTGT 1260

Qy      1273  CCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTAGTATCTGGAAAA 1332
                    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1261  CCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTAGTATCTGGAAAA 1320

Qy      1333  ATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTGAACCCTATTGGT 1392
                    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1321  ATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTGAACCCTATTGGT 1380

Qy      1393  GTTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAGTTTGACTGGTTC 1452
                    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1381  GTTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAGTTTGACTGGTTC 1440

Qy      1453  AGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCCAATTGGTCTGTA 1512
                    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Db      1441  AGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCCAATTGGTCTGTA  1500

Qy      1513  TCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGACTAGCTAGAGAC  1572
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1501  TCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGACTAGCTAGAGAC  1560

Qy      1573  AATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAAATCCTCTC  1632
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db      1561  AATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACACGAGATCCTCTC  1620

Qy      1633  TCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGTGTAACT  1692
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1621  TCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGTGTAACT  1680

Qy      1693  ATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCTAGAGATGAAGTA  1752
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1681  ATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCTAGAGATGAAGTA  1740

Qy      1753  GCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCTATGGAA  1812
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1741  GCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCTATGGAA  1800

Qy      1813  CTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCGGTGCTTGGAA  1872
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1801  CTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCGGTGCTTGGAA  1860

Qy      1873  AAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGGTCCTAAAA  1932
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1861  AAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGGTCCTAAAA  1920

Qy      1933  TATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAAGCATTGACTAAT  1992
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1921  TATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAAGCATTGACTAAT  1980

Qy      1993  CAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCACAATAAAACAGTT  2052
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1981  CAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCACAATAAAACAGTT  2040

Qy      2053  AGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGGATGTATTTGAAG  2112
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2041  AGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGGATGTATTTGAAG  2100

Qy      2113  CACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACTTAACTGACATTCTCAAA  2172
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2101  CACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACTTAACTGACATTCTCAAA  2160

Qy      2173  CAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTTGAGCAAATGAGG  2232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2161  CAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTTGAGCAAATGAGG  2220
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Qy    2233 CGACCAGATTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAACCCTGCTCATCAA 2292
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2221 CGACCAGATTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAACCCTGCTCATCAA 2280

Qy    2293 CTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAAGGCCACTGTGG 2352
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2281 CTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAAGGCCACTGTGG 2340

Qy    2353 TTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAACAATGAGATCATC 2412
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2341 TTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAACAATGAGATCATC 2400

Qy    2413 TTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATTATTCGTATTATG 2472
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2401 TTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATTATTCGTATTATG 2460

Qy    2473 GAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTATGGTTGTCTGTCA 2532
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2461 GAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTATGGTTGTCTGTCA 2520

Qy    2533 ATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACTATTATGCAAATT 2592
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2521 ATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACTATTATGCAAATT 2580

Qy    2593 CAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACTACATCAGTGG 2652
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2581 CAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACTACATCAGTGG 2640

Qy    2653 CTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTGTTTACACGTTCA 2712
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2641 CTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTGTTTACACGTTCA 2700

Qy    2713 TGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGTCACAATAGTAAC 2772
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2701 TGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGTCACAATAGTAAC 2760

Qy    2773 ATCATGGTGAAAGACGATGGACAACTGTTTCATATAGATTTTGGACACTTTTTGGATCAC 2832
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2761 ATCATGGTGAAAGACGATGGACAACTGTTTCATATAGATTTTGGACACTTTTTGGATCAC 2820

Qy    2833 AAGAAGAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTGACACAGGATTTC 2892
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2821 AAGAAGAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTGACACAGGATTTC 2880

Qy    2893 TTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAATTTGAGAGGTTT 2952
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2881 TTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAATTTGAGAGGTTT 2940
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Qy    2953  CAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAATCTCTTCATAAAT 3012
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2941  CAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAATCTCTTCATAAAT 3000

Qy    3013  CTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTTGATGACATTGCA 3072
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3001  CTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTTGATGACATTGCA 3060

Qy    3073  TACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTGGAGTATTTCATG 3132
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3061  TACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTGGAGTATTTCATG 3120

Qy    3133  AAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGATTGGATCTTCCAC 3192
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3121  AAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGATTGGATCTTCCAC 3180

Qy    3193  ACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAAGCTCACTCTGGA 3252
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3181  ACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAAGCTCACTCTGGA 3240

Qy    3253  TTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCATAGGAATTGCAC 3312
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3241  TTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCATAGGAATTGCAC 3300

Qy    3313  AATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACTATATAATTTAAA 3372
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3301  AATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACTATATAATTTAAA 3360

Qy    3373  TAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATTTCAAAA 3424
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3361  TAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATTTCAAAA 3412
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RESULT 10
ADU05935
ID   ADU05935 standard; DNA; 3423 BP.
XX
AC   ADU05935;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Novel bronchial cancer-associated human gene SeqID157.
XX
KW   bronchial cancer; cytostatic; tumour-associated protein;
KW   cancer detection; metastasis; tumour; gene; ds; human.
XX
OS   Homo sapiens.
XX
PN   DE10316701-A1.
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XX
PD    04-NOV-2004.
XX
PF    09-APR-2003; 2003DE-01016701.
XX
PR    09-APR-2003; 2003DE-01016701.
XX
PA    (HINZ/) HINZMANN B.
PA    (HERM/) HERMANN K.
PA    (CAST/) HEIDEN CASTANOS-VELEZ E.
XX
PI    Mennerich D, Bruemmendorf T, Heiden E, Hermann K, Kinnemann H;
PI    Li X, Roepcke S, Staub E, Hinzmann B, Rosenthal A, Pilarsky C;
XX
DR    WPI; 2004-786403/78.
DR    P-PSDB; ADU06422.
XX
PT    New nucleic acid, and derived proteins, useful for diagnosis of bronchial
PT    cancer and in screening for therapeutic and diagnostic agents.
XX
PS    Claim 1; SEQ ID NO 157; 1381pp; German.
XX
CC    This invention relates to a novel isolated nucleic acid associated with
CC    bronchial cancer comprising 489 defined sequences given in the
CC    specification. The invention may be useful for the production of
CC    compounds with a cytostatic activity through the inhibition of expression
CC    or activity of tumour-associated proteins. The novel DNA sequences and
CC    the proteins/peptides encoded by them are used for detecting bronchial
CC    cancer or determining the risk of developing it and to screen for
CC    specific binding partners of the DNA or protein sequences, where the
CC    binding partners are potentially useful as agents for treating or
CC    diagnosing bronchial cancer. The DNA or protein sequences can also be
CC    used for prognosis, detection of metastases and for secondary treatment
CC    (of tumours that have been stabilised or are no longer detectable).
CC    Detecting abnormal expression of the DNA sequences provides early
CC    diagnosis of bronchial cancers. The present sequence is that of a novel
CC    bronchial cancer-associated human gene sequence of the invention.
XX
SQ    Sequence 3423 BP; 1134 A; 618 C; 709 G; 962 T; 0 U; 0 Other;

     Query Match              99.6%;   Score 3410.4;   DB 3;   Length 3423;
     Best Local Similarity    99.9%;
     Matches 3422;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG 60

Qy         61 CCCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC 120
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            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61  CCCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC  120

Qy     121  CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121  CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC  180

Qy     181  CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181  CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA  240

Qy     241  GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241  GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAA  300

Qy     301  CCATTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAGATCCTCAATCGAGAA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301  CCATTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAGATCCTCAATCGAGAA  360

Qy     361  ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361  ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA  420

Qy     421  CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421  CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTT  480

Qy     481  AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481  AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG  540

Qy     541  CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTA  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541  CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTA  600

Qy     601  ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601  ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG  660

Qy     661  CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAAACTAGAAGTATGTTGCTATCATCT  720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661  CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAAACTAGAAGTATGTTGCTATCATCT  720

Qy     721  GAACAATTAAAACTCTGTGTTTTAGAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGA  780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721  GAACAATTAAAACTCTGTGTTTTAGAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGA  780

Qy     781  TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT  840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      781  TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT  840

Qy      841  ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAGCCTTTATTCTCAA   900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841  ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAGCCTTTATTCTCAA   900

Qy      901  CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA   960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901  CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA   960

Qy      961  TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961  TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA  1020

Qy     1021  AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT  1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021  AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT  1080

Qy     1081  CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA  1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081  CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA  1140

Qy     1141  CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTT  1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1141  CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTT  1200

Qy     1201  CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA  1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1201  CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA  1260

Qy     1261  GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA  1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1261  GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA  1320

Qy     1321  GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG  1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1321  GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG  1380

Qy     1381  AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAACTCCATGCTTAGAGTTGGAG  1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1381  AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAACTCCATGCTTAGAGTTGGAG  1440

Qy     1441  TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC  1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1441  TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC  1500

Qy     1501  AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA  1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1501  AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA  1560
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Qy   1561  CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA  1620
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561  CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA  1620

Qy   1621  CGAAATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC  1680
            |||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621  CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC  1680

Qy   1681  TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT  1740
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681  TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT  1740

Qy   1741  AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAGATTGGCCTCCAATCAAACCTGAA  1800
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741  AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAGATTGGCCTCCAATCAAACCTGAA  1800

Qy   1801  CAGGCTATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT  1860
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801  CAGGCTATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT  1860

Qy   1861  CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA  1920
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861  CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA  1920

Qy   1921  CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA  1980
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921  CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA  1980

Qy   1981  GCATTGACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCAC  2040
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981  GCATTGACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCAC  2040

Qy   2041  AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG  2100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041  AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG  2100

Qy   2101  ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAGCTCATTAACTTAACT  2160
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101  ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAGCTCATTAACTTAACT  2160

Qy   2161  GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT  2220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161  GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT  2220

Qy   2221  GAGCAAATGAGGCGACCAGATTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC  2280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221  GAGCAAATGAGGCGACCAGATTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC  2280
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Qy      2281  CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAA  2340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2281  CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAA  2340

Qy      2341  AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC  2400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2341  AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC  2400

Qy      2401  AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT  2460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2401  AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT  2460

Qy      2461  ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT  2520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2461  ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT  2520

Qy      2521  GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT  2580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2521  GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT  2580

Qy      2581  ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA  2640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2581  ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA  2640

Qy      2641  CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG  2700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2641  CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG  2700

Qy      2701  TTTACACGTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT  2760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2701  TTTACACGTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT  2760

Qy      2761  CACAATAGTAACATCATGGTGAAAGACGATGGACAACTGTTTCATATAGATTTTGGACAC  2820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2761  CACAATAGTAACATCATGGTGAAAGACGATGGACAACTGTTTCATATAGATTTTGGACAC  2820

Qy      2821  TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG  2880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2821  TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG  2880

Qy      2881  ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA  2940
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2881  ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA  2940

Qy      2941  TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT  3000
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2941  TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT  3000

Qy      3001  CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT  3060
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               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3001   CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT 3060

Qy      3061   GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG 3120
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3061   GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG 3120

Qy      3121   GAGTATTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT 3180
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3121   GAGTATTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT 3180

Qy      3181   TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA 3240
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3181   TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA 3240

Qy      3241   GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA 3300
               ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db      3241   GCTCACTCTGGATTCCACACTGCACTG-TAATAACTCTCAGCAGGCAAAGACCGATTGCA 3299

Qy      3301   TAGGAATTGCACAATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACT 3360
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3300   TAGGAATTGCACAATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAATACT 3359

Qy      3361   ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATTTC 3420
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3360   ATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATTTC 3419

Qy      3421   AAAA 3424
               ||||
Db      3420   AAAA 3423
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RESULT 11
ARC02473
ID    ARC02473 standard; DNA; 3426 BP.
XX
AC    ARC02473;
XX
DT    10-JUL-2008  (first entry)
XX
DE    DNA fragments of a human Tox gene, 46524.
XX
KW    DNA microarray; gene expression; drug screening; ds; Tox.
XX
OS    Homo sapiens.
XX
PN    US2007072175-A1.
XX
PD    29-MAR-2007.

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XX
PF    15-MAY-2006; 2006US-00433832.
XX
PR    13-MAY-2005; 2005US-0680473P.
PR    13-MAY-2005; 2005US-0680544P.
XX
PA    (BIOJ ) BIOGEN IDEC MA INC.
XX
PI    Cooper MT,  Kinch D,  Rosenberg M,  Subramaniam SS,  Szak ST,  Li H;
PI    Bandaru R,  Derbel M;
XX
DR    WPI; 2007-432796/41.
XX
PT    New nucleotide array comprises polynucleotide probes complementary to, or
PT    fragments of, Cynomolgus monkey genes, useful for detecting changes in
PT    gene expression upon administration of a therapeutic agent.
XX
PS    Claim 18; SEQ ID NO 46524; 33pp; English.
XX
CC    The new invention relates to a nucleotide array for detecting changes in
CC    gene expression upon administration of a therapeutic agent. The
CC    microarray has polynucleotide probes complementary to, or fragments of,
CC    Cynomolgus monkey genes, where each polynucleotide probe is immobilized
CC    to a discrete and known spot on a solid support. The polynucleotide
CC    probes are complementary to, or fragments of, any portion of an ortholog
CC    of a human gene, preferably a Tox gene. The probes are any of SEQ ID NO.
CC    8882-9186. The probes are also complementary to, or fragments of, any
CC    portion of any of SEQ ID NO. 1-8881 or 9187-18598. The nucleotide array
CC    has at least one probe complementary to, or a fragment of, any portion of
CC    any human gene, where the probe from a human gene is any of SEQ ID NO.
CC    43226-48714, or is complementary to, or a fragment of, any portion of any
CC    of SEQ ID NO. 43450-48714. The array has at least one probe complementary
CC    to, or a fragment of, any portion of any Rhesus monkey gene, where the
CC    probe from a Rhesus monkey gene is any of SEQ ID NO. 35841-36074, or is
CC    complementary to, or a fragment of, any portion of any of SEQ ID NO.
CC    18599-35840 or 36075-43225. It also has at least one probe complementary
CC    to, or a fragment of, any portion of a Rhesus monkey gene and at least
CC    one probe complementary to, or a fragment of, any portion of any human
CC    gene. The nucleotide array is useful for detecting changes in gene
CC    expression upon administration of a therapeutic agent. It can be used for
CC    characterizing the actions, targets, and toxicities of therapeutic agents
CC    in primates, e.g. a human, a Cynomolgus monkey, or a Rhesus monkey. This
CC    sequence is a DNA fragment of a human Tox gene.
XX
SQ    Sequence 3426 BP; 1138 A; 623 C; 703 G; 962 T; 0 U; 0 Other;

   Query Match             97.5%;  Score 3338;  DB 6;  Length 3426;
   Best Local Similarity   98.8%;
   Matches 3384;  Conservative    0;  Mismatches   40;  Indels    2;  Gaps    2;
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Qy      1   AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG   60
            | |  | | | | | | | | | | | | | | | | | | |   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1   AGAATCAGAACAATGCCTCCACGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG   60

Qy     61   CCCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC   120
            | | | | | | | | | | | | | | | | | | |   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     61   CCCCCAAGAATCCTAGTAGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC   120

Qy    121   CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC   180
            | | | | | | | | | | | | | | | |   | | |  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    121   CTCCGTGAGGCTACATTAATAACCATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC   180

Qy    181   CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA   240
            | |  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |   | | | | | |
Db    181   CCCCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACTCAAGAA   240

Qy    241   GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAA   300
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  | | | | | | | | | | | | | | | | |
Db    241   GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGACCTTCGGCTTTTTCAA   300

Qy    301   CCATTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA   360
            | |  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    301   CCCTTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA   360

Qy    361   ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA   420
            | | | | | | | | | | | | | | | | | | | | | | | | | | |  | | | | | | | | | | | | | | | | | | | | | |   | | | | | |
Db    361   ATTGGTTTTGCTATCGGCATGCCAGTGTGTGAATTTGATATGGTTAAAGATCCAGAAGTA   420

Qy    421   CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTT   480
            | | | | | | | | | | | | | | | | | | | | |  | |  | | | | | | | | | | | | | | | | | | | | | | | | | | |   | |
Db    421   CAGGACTTCCGAAGAAATATTCTGAACGTTTGTAAAGAAGCTGTGGATCTTAGGGACCTC   480

Qy    481   AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG   540
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  | | |  | | | | | | | | | | | | | | | | | | |
Db    481   AATTCACCTCATAGTAGAGCAATGTATGTCTATCCTCCAAATGTAGAATCTTCACCAGAA   540

Qy    541   CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTA   600
            | | | | | | | | | | | | | | | | | | | | | | | | |  | | | |   | | |   | | | | | | | | | | | | | | | | | |   | | | | | |
Db    541   TTGCCAAAGCACATATATAATAAATTAGATAAAGGGCAAATAATAGTGGTGATCTGGGTA   600

Qy    601   ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG   660
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    601   ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTA   660

Qy    661   CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAAACTAGAAGTATGTTGCTATCATCT   720
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  | | | | | | | | | | | | | | |   | | |
Db    661   CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAAACTCGAAGTATGTTGCTATCCTCT   720
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Qy       721  GAACAATTAAAACTCTGTGTTTTAGAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGA  780
              ||||||| ||||||||||||||||||||||||||||||||||| || |||||||||||||
Db       721  GAACAACTAAAACTCTGTGTTTTAGAATATCAGGGCAAGTATATTTTAAAAGTGTGTGGA  780

Qy       781  TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT  840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781  TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT  840

Qy       841  ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA  900
              |||||||||||||||||||||||||||||| | ||||||||||||||||||||||||||||
Db       841  ATAATGCTTGGGAGGATGCCCAATTTGATGTTGATGGCTAAAGAAAGCCTTTATTCTCAA  900

Qy       901  CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA  960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901  CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA  960

Qy       961  TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA  1020
              |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db       961  TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGTGCACTCAGAATA  1020

Qy      1021  AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT  1080
              ||||||||||||||||||||||||||||| |||||||||||||||||| ||||| ||||||
Db      1021  AAAATTCTTTGTGCAACCTACGTGAATGTAAATATTCGAGACATTGATAAGATCTATGTT  1080

Qy      1081  CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA  1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081  CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA  1140

Qy      1141  CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTT  1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141  CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTT  1200

Qy      1201  CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA  1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201  CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA  1260

Qy      1261  GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA  1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261  GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA  1320

Qy      1321  GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG  1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321  GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG  1380

Qy      1381  AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAG  1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381  AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAG  1440

Qy      1441  TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC  1500
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                    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1441   TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC   1500

Qy      1501   AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA   1560
                    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1501   AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA   1560

Qy      1561   CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA   1620
                    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1561   CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA   1620

Qy      1621   CGAAATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC   1680
                    | | |     | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1621   CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC   1680

Qy      1681   TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT   1740
                    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1681   TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT   1740

Qy      1741   AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA   1800
                    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1741   AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA   1800

Qy      1801   CAGGCTATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT   1860
                    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1801   CAGGCTATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT   1860

Qy      1861   CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA   1920
                    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1861   CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA   1920

Qy      1921   CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA   1980
                    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1921   CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA   1980

Qy      1981   GCATTGACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCAC   2040
                    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1981   GCATTGACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCAC   2040

Qy      2041   AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG   2100
                    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2041   AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG   2100

Qy      2101   ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACTTAACT   2160
                    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2101   ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACTTAACT   2160

Qy      2161   GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT   2220
                    | | | | | | | | | | | | | | | | | | |     | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Db     2161  GACATTCTCAAACAGGAGAAGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT 2220

Qy     2221  GAGCAAATGAGGCGACCAGATTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC 2280
             | | | | | | | | | | | | | | | | | | | | | | | | | | | |   | | | | | | | | | | | |   | | | | | | | | | |
Db     2221  GAGCAAATGAGGCGACCAGATTTCATGGATGCTCTACAGGGCTTTCTGTCTCCTCTAAAC 2280

Qy     2281  CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAA 2340
             | | | | | | | | | | | | | | | | | | | | | | | | | | |   | | | | | | | | | | | | | | | | | | |   | | | | | | | | |
Db     2281  CCTGCTCATCAACTAGGAAACCTCAGGCTTGAAGAGTGTCGAATTATGTCCTCTGCAAAA 2340

Qy     2341  AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC 2400
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     2341  AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC 2400

Qy     2401  AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT 2460
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     2401  AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT 2460

Qy     2461  ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT 2520
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     2461  ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT 2520

Qy     2521  GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT 2580
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     2521  GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT 2580

Qy     2581  ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA 2640
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     2581  ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA 2640

Qy     2641  CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG 2700
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     2641  CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG 2700

Qy     2701  TTTACACGTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT 2760
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     2701  TTTACACGTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT 2760

Qy     2761  CACAATAGTAACATCATGGTGAAAGACGATGGACAACTGTTTCATATAGATTTTGGACAC 2820
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     2761  CACAATAGTAACATCATGGTGAAAGACGATGGACAACTGTTTCATATAGATTTTGGACAC 2820

Qy     2821  TTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG 2880
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     2821  TTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG 2880

Qy     2881  ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA 2940
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     2881  ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA 2940
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Qy      2941  TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT  3000
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2941  TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT  3000

Qy      3001  CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT  3060
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3001  CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT  3060

Qy      3061  GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG  3120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3061  GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG  3120

Qy      3121  GAGTATTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT  3180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3121  GAGTATTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT  3180

Qy      3181  TGGATCTTCCACACAATTAAACAGCATGCATTGAACTG-AAAGATAACTGAGAAATGAA   3239
              |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db      3181  TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAAGATAACTGAGAAATGAA   3240

Qy      3240  AGCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGC  3299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3241  AGCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGC  3300

Qy      3300  ATAGGAATTGCACAATCCATGAACAGCATTAG-ATTTACAGCAAGAACAGAAATAAAATA  3358
              |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db      3301  ATAGGAATTGCACAATCCATGAACAGCATTAGAATTTACAGCAAGAACAGAAATAAAATA  3360

Qy      3359  CTATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATT  3418
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3361  CTATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATT  3420

Qy      3419  TCAAAA  3424
              ||||||
Db      3421  TCAAAA  3426
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RESULT 12
AEK54940
ID    AEK54940 standard; DNA; 3724 BP.
XX
AC    AEK54940;
XX
DT    11-JUN-2007  (revised)
DT    16-NOV-2006  (first entry)
XX
DE    Human PIK3CA DNA, SEQ ID NO:7.
XX
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KW    phosphoinositide-3-kinase, catalytic, alpha; PIK3CA; genetic marker;
KW    screening; adenocarcinoma; neoplasm; cytostatic; ds.
XX
OS    Homo sapiens.
XX
PN    WO2006094149-A2.
XX
PD    08-SEP-2006.
XX
PF    01-MAR-2006; 2006WO-US007493.
XX
PR    01-MAR-2005; 2005US-0657841P.
XX
PA    (EXAC-) EXACT SCI CORP.
XX
PI    Shuber AP;
XX
DR    WPI; 2006-680485/70.
DR    REFSEQ; NM_006218.
DR    PC:NCBI; gi54792081.
DR    PC_ENCPRO:NCBI; gi54792082.
XX
PT    Screening for adenoma in a subject, comprises testing a sample for the
PT    presence of each of a panel of genetic markers, where the panel is more
PT    than 60% informative for adenoma.
XX
PS    Disclosure; SEQ ID NO 7; 79pp; English.
XX
CC    The invention relates to a method for screening a subject for the
CC    presence of adenoma. The method comprises interrogating a sample from the
CC    subject for each of a panel of genetic markers, where the panel is more
CC    than 60% informative for adenoma, and where the presence of one or more
CC    of the markers is indicative of adenoma. Also described are: (1) a method
CC    of detecting indicia of adenoma, by assaying a sample from a subject for
CC    the presence of one or more genetic abnormalities from a group of genetic
CC    abnormalities that is more than 60% informative for adenoma; (2) a method
CC    of detecting adenoma in a subject, by performing an assay on a sample
CC    from the subject that is more than 60% informative for adenoma; and (3) a
CC    kit comprising a group of oligonucleotides, where each oligonucleotide is
CC    adapted for interrogating a genetic locus for the presence of a marker
CC    from a panel that is at least 60% informative for adenoma. The methods
CC    and kit of the invention are useful for screening for adenoma in a
CC    subject. The adenoma is especially a colonic and/or invasive adenoma. The
CC    methods can detect adenoma at an early stage with a high level of
CC    confidence, increasing the chances of successful treatment. This sequence
CC    represents a human DNA sequence that can be used as a genetic marker in
CC    the method of the invention.
CC
CC    Revised record issued on 11-JUN-2007 : Enhanced with precomputed
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CC    information from BOND.
XX
SQ    Sequence 3724 BP; 1242 A; 684 C; 763 G; 1035 T; 0 U; 0 Other;

    Query Match           97.5%;   Score 3338;   DB 4;   Length 3724;
    Best Local Similarity  98.8%;
    Matches 3384;  Conservative   0;  Mismatches  40;  Indels   2;  Gaps   2;

Qy         1 AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG 60
             || ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db       146 AGAATCAGAACAATGCCTCCACGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG 205

Qy        61 CCCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC 120
             ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db       206 CCCCCAAGAATCCTAGTAGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC 265

Qy       121 CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC 180
             |||||||||||||||||| |||| |||||||||||||||||||||||||||||||||||
Db       266 CTCCGTGAGGCTACATTAATAACCATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC 325

Qy       181 CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA 240
             || ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db       326 CCCCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACTCAAGAA 385

Qy       241 GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAA 300
             ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db       386 GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGACCTTCGGCTTTTTCAA 445

Qy       301 CCATTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA 360
             || |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       446 CCCTTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA 505

Qy       361 ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA 420
             |||||||||||||||||||||||||||||||| |||||||||||||||||||| ||||||
Db       506 ATTGGTTTTGCTATCGGCATGCCAGTGTGTGAATTTGATATGGTTAAAGATCCAGAAGTA 565

Qy       421 CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTT 480
             ||||||||||||||||||||||| || |||||||||||||||||||||||||||| ||
Db       566 CAGGACTTCCGAAGAAATATTCTGAACGTTTGTAAAGAAGCTGTGGATCTTAGGGACCTC 625

Qy       481 AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG 540
             |||||||||||||||||||||||||||||||||||| ||| |||||||||||||||||||
Db       626 AATTCACCTCATAGTAGAGCAATGTATGTCTATCCTCCAAATGTAGAATCTTCACCAGAA 685

Qy       541 CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTA 600
             |||||||||||||||||||||||||| |||| ||| |||||||||||||||||| ||||||
Db       686 TTGCCAAAGCACATATATAATAAATTAGATAAAGGGCAAATAATAGTGGTGATCTGGGTA 745

Qy       601 ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG 660
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                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       746    ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTA  805

Qy       661    CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT   720
                ||||||||||||||||||||||||||||||||||||||||| |||||||||||||  |||   |||
Db       806    CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTCGAAGTATGTTGCTATCCTCT   865

Qy       721    GAACAATTAAAACTCTGTGTTTTAGAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGA   780
                ||||||  ||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db       866    GAACAACTAAAACTCTGTGTTTTAGAATATCAGGGCAAGTATATTTTAAAAGTGTGTGGA   925

Qy       781    TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT   840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       926    TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT   985

Qy       841    ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA   900
                ||||||||||||||||||||||||||||||||  | ||||||||||||||||||||||||
Db       986    ATAATGCTTGGGAGGATGCCCAATTTGATGTTGATGGCTAAAGAAAGCCTTTATTCTCAA  1045

Qy       901    CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA   960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1046    CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA  1105

Qy       961    TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA  1020
                ||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||||
Db      1106    TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGTGCACTCAGAATA  1165

Qy      1021    AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT  1080
                ||||||||||||||||||||||||||||| |||||||||||||||||||  ||||| ||||||
Db      1166    AAAATTCTTTGTGCAACCTACGTGAATGTAAATATTCGAGACATTGATAAGATCTATGTT  1225

Qy      1081    CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA  1140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1226    CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA  1285

Qy      1141    CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATACATTCCTGATCTT  1200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1286    CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATACATTCCTGATCTT  1345

Qy      1201    CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA  1260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1346    CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA  1405

Qy      1261    GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA  1320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1406    GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA  1465

Qy      1321    GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG  1380
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    1466  GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG  1525


Qy    1381  AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAG  1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1526  AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAG  1585


Qy    1441  TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC  1500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1586  TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC  1645


Qy    1501  AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA  1560
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1646  AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA  1705


Qy    1561  CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA  1620
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1706  CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA  1765


Qy    1621  CGAAATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC  1680
            |||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1766  CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC  1825


Qy    1681  TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT  1740
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1826  TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT  1885


Qy    1741  AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA  1800
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1886  AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA  1945


Qy    1801  CAGGCTATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT  1860
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1946  CAGGCTATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT  2005


Qy    1861  CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA  1920
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2006  CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA  2065


Qy    1921  CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA  1980
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2066  CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA  2125


Qy    1981  GCATTGACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCAC  2040
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2126  GCATTGACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCAC  2185


Qy    2041  AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG  2100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2186  AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG  2245
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Qy    2101  ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACTTAACT  2160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2246  ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACTTAACT  2305

Qy    2161  GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT  2220
            |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    2306  GACATTCTCAAACAGGAGAAGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT  2365

Qy    2221  GAGCAAATGAGGCGACCAGATTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC  2280
            ||||||||||||||||||||||||||||||||||| ||||||||| ||||||||||||||
Db    2366  GAGCAAATGAGGCGACCAGATTTCATGGATGCTCTACAGGGCTTTCTGTCTCCTCTAAAC  2425

Qy    2281  CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAA  2340
            ||||||||||||||||||||||||||||||||| |||||||||||||||| |||||||||
Db    2426  CCTGCTCATCAACTAGGAAACCTCAGGCTTGAAGAGTGTCGAATTATGTCCTCTGCAAAA  2485

Qy    2341  AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC  2400
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2486  AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC  2545

Qy    2401  AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT  2460
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2546  AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT  2605

Qy    2461  ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT  2520
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2606  ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT  2665

Qy    2521  GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT  2580
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2666  GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT  2725

Qy    2581  ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA  2640
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2726  ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA  2785

Qy    2641  CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG  2700
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2786  CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG  2845

Qy    2701  TTTACACGTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT  2760
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2846  TTTACACGTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT  2905

Qy    2761  CACAATAGTAACATCATGGTGAAAGACGATGGACAACTGTTTCATATAGATTTTGGACAC  2820
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2906  CACAATAGTAACATCATGGTGAAAGACGATGGACAACTGTTTCATATAGATTTTGGACAC  2965
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Qy      2821 TTTTTGGATCACAAGAAGAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG 2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2966 TTTTGGATCACAAGAAGAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG 3025

Qy      2881 ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA 2940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3026 ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA 3085

Qy      2941 TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT 3000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3086 TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT 3145

Qy      3001 CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT 3060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3146 CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT 3205

Qy      3061 GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG 3120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3206 GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG 3265

Qy      3121 GAGTATTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT 3180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3266 GAGTATTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT 3325

Qy      3181 TGGATCTTCCACACAATTAAACAGCATGCATTGAACTG-AAAGATAACTGAGAAAATGAA 3239
             ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db      3326 TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAAGATAACTGAGAAAATGAA 3385

Qy      3240 AGCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGC 3299
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3386 AGCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGC 3445

Qy      3300 ATAGGAATTGCACAATCCATGAACAGCATTAG-ATTTACAGCAAGAACAGAAATAAAATA 3358
             |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db      3446 ATAGGAATTGCACAATCCATGAACAGCATTAGAATTTACAGCAAGAACAGAAATAAAATA 3505

Qy      3359 CTATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATT 3418
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3506 CTATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATT 3565

Qy      3419 TCAAAA 3424
             ||||||
Db      3566 TCAAAA 3571
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RESULT 13
AER29796
ID   AER29796 standard; DNA; 3724 BP.
XX
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AC      AER29796;
XX
DT      11-JUN-2007  (revised)
DT      22-MAR-2007  (first entry)
XX
DE      Breast cancer-associated gene SEQ ID NO:97.
XX
KW      diagnosis; breast tumor; biochip; tumor marker; genetic marker;
KW      biomarker; DNA detection; RNA detection; ds; PIK3CA.
XX
OS      Homo sapiens.
XX
PN      WO2007006911-A2.
XX
PD      18-JAN-2007.
XX
PF      05-JUL-2006; 2006WO-FR001593.
XX
PR      07-JUL-2005; 2005FR-00052087.
XX
PA      (INMR ) BIOMERIEUX SA.
XX
PI      Krause A,  Leissner P,  Mougin B,  Paye M;
XX
DR      WPI; 2007-138577/14.
DR      PC:NCBI; gi54792081.
DR      PC_ENCPRO:NCBI; gi54792082.
XX
PT      In vitro diagnosis of breast cancer comprises extracting biological
PT      material of biological sample, contacting biological material with
PT      specific reagents of target genes and determining target gene expression.
XX
PS      Example 2; SEQ ID NO 97; 305pp; French.
XX
CC      The invention describes a method for in vitro diagnosis of breast cancer
CC      in a patient susceptible to be affected by breast cancer, comprising:
CC      extracting nucleic acid from a biological sample taken from the patient;
CC      contacting the nucleic acid with at least 8 hybridization probes for
CC      detection of target genes chosen from SEQ ID Nos. 1 to 8 or 10 probes for
CC      detection of target genes chosen from SEQ ID Nos. 1, 2, 4, 6, 13, 14, 26,
CC      69, 81 and 105; and determining the expression of the target genes. The
CC      invention also includes: a support, such as a biochip, comprising at
CC      least 8 or 10 hybridization probes mentioned above; and a diagnosis kit
CC      for breast cancer comprising the support. The method, biochip and kit are
CC      useful for the in vitro diagnosis of breast cancer. This sequence is a
CC      breast cancer-associated gene.
CC
CC      Revised record issued on 11-JUN-2007 : Enhanced with precomputed
CC      information from BOND.
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XX
SQ    Sequence 3724 BP; 1242 A; 684 C; 763 G; 1035 T; 0 U; 0 Other;

   Query Match                   97.5%;   Score 3338;   DB 5;   Length 3724;
   Best Local Similarity   98.8%;
   Matches 3384;  Conservative     0;  Mismatches    40;  Indels     2;  Gaps      2;


Qy         1 AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG 60
             || |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       146 AGAATCAGAACAATGCCTCCACGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG 205


Qy        61 CCCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC 120
             ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db       206 CCCCCAAGAATCCTAGTAGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC 265


Qy       121 CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC 180
             ||||||||||||||||||| |||| |||||||||||||||||||||||||||||||||||
Db       266 CTCCGTGAGGCTACATTAATAACCATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC 325


Qy       181 CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA 240
             ||  |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db       326 CCCCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACTCAAGAA 385


Qy       241 GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAA 300
             ||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db       386 GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGACCTTCGGCTTTTTCAA 445


Qy       301 CCATTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA 360
             ||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       446 CCCTTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA 505


Qy       361 ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA 420
             |||||||||||||||||||||||||||||||| |||||||||||||||||||||| ||||||
Db       506 ATTGGTTTTGCTATCGGCATGCCAGTGTGTGAATTTGATATGGTTAAAGATCCAGAAGTA 565


Qy       421 CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTT 480
             |||||||||||||||||||||||| || ||||||||||||||||||||||||||||| ||
Db       566 CAGGACTTCCGAAGAAATATTCTGAACGTTTGTAAAGAAGCTGTGGATCTTAGGGACCTC 625


Qy       481 AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG 540
             |||||||||||||||||||||||||||||||||||| ||| |||||||||||||||||||
Db       626 AATTCACCTCATAGTAGAGCAATGTATGTCTATCCTCCAAATGTAGAATCTTCACCAGAA 685


Qy       541 CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTA 600
             |||||||||||||||||||||||||||| |||| ||| |||||||||||||||||| ||||||
Db       686 TTGCCAAAGCACATATATAATAAATTAGATAAAGGGCAAATAATAGTGGTGATCTGGGTA 745


Qy       601 ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG 660
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      746  ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTA  805

Qy      661  CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT  720
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |   | | | | | | | | | | | | |   | | |
Db      806  CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTCGAAGTATGTTGCTATCCTCT  865

Qy      721  GAACAATTAAAACTCTGTGTTTTAGAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGA  780
             | | | | | |   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |   | | | | | | | | | | | | | | | |
Db      866  GAACAACTAAAACTCTGTGTTTTAGAATATCAGGGCAAGTATATTTTAAAAGTGTGTGGA  925

Qy      781  TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT  840
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      926  TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT  985

Qy      841  ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA  900
             | | | | | | | | | | | | | | | | | | | | | | | | |   |   | | | | | | | | | | | | | | | | | | | | | | | | |
Db      986  ATAATGCTTGGGAGGATGCCCAATTTGATGTTGATGGCTAAAGAAAGCCTTTATTCTCAA  1045

Qy      901  CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA  960
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     1046  CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA  1105

Qy      961  TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA  1020
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |   | | | | | | | | | | | |
Db     1106  TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGTGCACTCAGAATA  1165

Qy     1021  AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT  1080
             | | | | | | | | | | | | | | | | | | | | | |   | | | | | | | | | | | | | | | | | | | |   | | | | |   | | | | | |
Db     1166  AAAATTCTTTGTGCAACCTACGTGAATGTAAATATTCGAGACATTGATAAGATCTATGTT  1225

Qy     1081  CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA  1140
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     1226  CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA  1285

Qy     1141  CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTT  1200
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     1286  CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTT  1345

Qy     1201  CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA  1260
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     1346  CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA  1405

Qy     1261  GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA  1320
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     1406  GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA  1465

Qy     1321  GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG  1380
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     1466  GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG  1525
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Qy    1381  AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAG  1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1526  AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAG  1585

Qy    1441  TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC  1500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1586  TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC  1645

Qy    1501  AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA  1560
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1646  AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA  1705

Qy    1561  CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA  1620
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1706  CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA  1765

Qy    1621  CGAAATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC  1680
            |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1766  CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC  1825

Qy    1681  TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT  1740
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1826  TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT  1885

Qy    1741  AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAGATTGGCCTCCAATCAAACCTGAA  1800
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1886  AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAGATTGGCCTCCAATCAAACCTGAA  1945

Qy    1801  CAGGCTATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT  1860
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1946  CAGGCTATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT  2005

Qy    1861  CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA  1920
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2006  CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA  2065

Qy    1921  CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA  1980
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2066  CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA  2125

Qy    1981  GCATTGACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCAC  2040
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2126  GCATTGACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCAC  2185

Qy    2041  AATAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG  2100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2186  AATAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG  2245
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Qy      2101 ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACTTAACT 2160
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2246 ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACTTAACT 2305

Qy      2161 GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT 2220
             |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db      2306 GACATTCTCAAACAGGAGAAGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT 2365

Qy      2221 GAGCAAATGAGGCGACCAGATTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC 2280
             ||||||||||||||||||||||||||||||||| |||||||||| |||||||||||||||
Db      2366 GAGCAAATGAGGCGACCAGATTTCATGGATGCTCTACAGGGCTTTCTGTCTCCTCTAAAC 2425

Qy      2281 CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAA 2340
             |||||||||||||||||||||||||||||||| |||||||||||||||||| ||||||||
Db      2426 CCTGCTCATCAACTAGGAAACCTCAGGCTTGAAGAGTGTCGAATTATGTCCTCTGCAAAA 2485

Qy      2341 AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2486 AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC 2545

Qy      2401 AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2546 AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT 2605

Qy      2461 ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2606 ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT 2665

Qy      2521 GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2666 GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT 2725

Qy      2581 ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2726 ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA 2785

Qy      2641 CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2786 CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG 2845

Qy      2701 TTTACACGTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT 2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2846 TTTACACGTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT 2905

Qy      2761 CACAATAGTAACATCATGGTGAAAGACGATGGACAACTGTTTCATATAGATTTTGGACAC 2820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2906 CACAATAGTAACATCATGGTGAAAGACGATGGACAACTGTTTCATATAGATTTTGGACAC 2965

Qy      2821 TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG 2880
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            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    2966  TTTTGGATCACAAGAAGAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG  3025

Qy    2881  ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA  2940
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    3026  ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA  3085

Qy    2941  TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT  3000
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    3086  TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT  3145

Qy    3001  CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT  3060
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    3146  CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT  3205

Qy    3061  GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG  3120
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    3206  GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG  3265

Qy    3121  GAGTATTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT  3180
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    3266  GAGTATTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT  3325

Qy    3181  TGGATCTTCCACACAATTAAACAGCATGCATTGAACTG-AAAGATAACTGAGAAAATGAA  3239
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    3326  TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAAGATAACTGAGAAAATGAA  3385

Qy    3240  AGCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGC  3299
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    3386  AGCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGC  3445

Qy    3300  ATAGGAATTGCACAATCCATGAACAGCATTAG-ATTTACAGCAAGAACAGAAATAAAATA  3358
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    3446  ATAGGAATTGCACAATCCATGAACAGCATTAGAATTTACAGCAAGAACAGAAATAAAATA  3505

Qy    3359  CTATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATT  3418
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    3506  CTATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATT  3565

Qy    3419  TCAAAA  3424
            | | | | | |
Db    3566  TCAAAA  3571
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RESULT 14
ARV60468
ID    ARV60468 standard; cDNA; 3724 BP.
XX
AC    ARV60468;

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XX
DT    24-JUL-2008  (first entry)
XX
DE    Human PIK3CA polynucleotide, SEQ ID 30.
XX
KW    mutation; dna microarray; prognosis; diagnostic test; therapeutic;
KW    non-small-cell lung cancer; tumor; cytostatic; ss; gene;
KW    phosphoinositide-3-kinase, catalytic, alpha polypeptide; PIK3CA.
XX
OS    Homo sapiens.
XX
FH    Key              Location/Qualifiers
FT    CDS              158. .3364
FT                     /*tag=   a
FT                     /product
XX
PN    WO2008061213-A2.
XX
PD    22-MAY-2008.
XX
PF    15-NOV-2007; 2007WO-US084888.
XX
PR    16-NOV-2006; 2006US-0866103P.
PR    10-JUL-2007; 2007US-0948818P.
XX
PA    (GETH ) GENENTECH INC.
XX
PI    Seshagiri S,  Peters B,  Kan Z;
XX
DR    WPI; 2008-G25985/39.
DR    P-PSDB; ARV60505.
DR    PC:NCBI; gi54792081.
DR    PC_ENCPRO:NCBI; gi54792082.
XX
PT    New isolated polynucleotide comprises PRO polynucleotide or fragment
PT    comprising a nucleotide variation, useful for detecting nucleotide
PT    variations for diagnosing and treating tumors.
XX
PS    Claim 2; SEQ ID NO 30; 55pp; English.
XX
CC    The present invention relates to a novel isolated polynucleotide
CC    comprising a PRO polynucleotide or its fragment. The PRO polynucleotide
CC    or its fragment comprises a nucleotide variation at a nucleotide position
CC    given in the specification. A nucleotide variation refers to a change in
CC    a nucleotide sequence (e.g., an insertion, deletion, inversion, or
CC    substitution of one or more nucleotides, such as a single nucleotide
CC    polymorphism (SNP)) relative to a reference sequence (e.g., a wild type
CC    sequence). A nucleotide variation may be a somatic mutation or a germline
CC    polymorphism. The present invention provides: (i) an allele-specific
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CC    oligonucleotide that hybridizes to a region of a PRO polynucleotide
CC    comprising a nucleotide variation at a nucleotide position, or its
CC    complement; (ii) a kit comprising the oligonucleotide and an enzyme;
CC    (iii) a microarray comprising the oligonucleotide; (iv) a method for
CC    detecting the absence or presence of the variation at a nucleotide
CC    position; (v) a method for amplifying a nucleic acid comprising the
CC    nucleotide variation; (vi) a method for determining the genotype of a
CC    biological sample (e.g. non-small cell lung carcinoma sample) from a
CC    mammal; (vii) a method for classifying a tumor in the mammal; and (viii)
CC    a method for predicting whether a tumor (e.g. non-small cell lung
CC    carcinoma) will respond to a therapeutic agent that targets a PRO or a
CC    PRO polynucleotide, comprises determining whether the tumor comprises a
CC    variation in a PRO or PRO polynucleotide, where the presence of a
CC    variation indicates that the tumor will respond to the therapeutic agent.
CC    The method of detecting the absence or presence of the nucleotide
CC    variation comprises: (a) contacting the suspected nucleic acid with the
CC    allele-specific oligonucleotide that is specific for the nucleotide
CC    variation, under conditions suitable for hybridization of the
CC    oligonucleotide to the nucleic acid; and (b) detecting the absence or
CC    presence of allele-specific hybridization. The method of amplifying the
CC    nucleic acid comprising the nucleotide variation comprises: (a)
CC    contacting the nucleic acid with a primer that hybridizes to the nucleic
CC    acid at 3' of the nucleotide variation; and (b) extending the primer to
CC    generate an amplification product comprising the nucleotide variation.
CC    The isolated polynucleotide is used for detecting nucleotide variations.
CC    The methods are used for diagnosing and treating tumors. The present
CC    sequence is a human PRO polynucleotide sequence used in the invention.
CC
CC    Revised record issued on 18-JUN-2008 : Enhanced with precomputed
CC    information from BOND.
XX
SQ    Sequence 3724 BP; 1242 A; 684 C; 763 G; 1035 T; 0 U; 0 Other;

   Query Match             97.5%;  Score 3338;  DB 7;  Length 3724;
   Best Local Similarity   98.8%;
   Matches 3384;  Conservative    0;  Mismatches   40;  Indels    2;  Gaps    2;

Qy        1 AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG 60
            || |||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db      146 AGAATCAGAACAATGCCTCCACGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG 205

Qy       61 CCCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC 120
            ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db      206 CCCCCAAGAATCCTAGTAGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC 265

Qy      121 CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC 180
            |||||||||||||||||| |||| |||||||||||||||||||||||||||||||||||
Db      266 CTCCGTGAGGCTACATTAATAACCATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC 325
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Qy    181  CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA  240
           ||  |||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db    326  CCCCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACTCAAGAA  385

Qy    241  GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAA  300
           |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db    386  GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGACCTTCGGCTTTTTCAA  445

Qy    301  CCATTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA  360
           ||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    446  CCCTTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA  505

Qy    361  ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA  420
           |||||||||||||||||||||||||||||| |||||||||||||||||||| |||||||
Db    506  ATTGGTTTTGCTATCGGCATGCCAGTGTGTGAATTTGATATGGTTAAAGATCCAGAAGTA  565

Qy    421  CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTT  480
           ||||||||||||||||||||||||  || |||||||||||||||||||||||||||  ||
Db    566  CAGGACTTCCGAAGAAATATTCTGAACGTTTGTAAAGAAGCTGTGGATCTTAGGGACCTC  625

Qy    481  AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG  540
           |||||||||||||||||||||||||||||||||||||  ||| |||||||||||||||||
Db    626  AATTCACCTCATAGTAGAGCAATGTATGTCTATCCTCCAAATGTAGAATCTTCACCAGAA  685

Qy    541  CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTA  600
           |||||||||||||||||||||||||| |||| ||| ||||||||||||||||| |||||
Db    686  TTGCCAAAGCACATATATAATAAATTAGATAAAGGGCAAATAATAGTGGTGATCTGGGTA  745

Qy    601  ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG  660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    746  ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTA  805

Qy    661  CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT  720
           ||||||||||||||||||||||||||||||||||||||| |||||||||||||||| |||
Db    806  CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTCGAAGTATGTTGCTATCCTCT  865

Qy    721  GAACAATTAAAACTCTGTGTTTTAGAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGA  780
           ||||||  ||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    866  GAACAACTAAAACTCTGTGTTTTAGAATATCAGGGCAAGTATATTTTAAAAGTGTGTGGA  925

Qy    781  TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT  840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    926  TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT  985

Qy    841  ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA  900
           ||||||||||||||||||||||||||| | |||||||||||||||||||||||||||||
Db    986  ATAATGCTTGGGAGGATGCCCAATTTGATGTTGATGGCTAAAGAAAGCCTTTATTCTCAA  1045

Qy    901  CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA  960
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          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1046 CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA 1105

Qy    961 TATATGAATGGAGAAACATCTACAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA 1020
          ||||||||||||||||||||||||||||||||||||||||||| |||||| |||||||||||
Db   1106 TATATGAATGGAGAAACATCTACAAATCCCTTTGGGTTATAAATAGTGCACTCAGAATA 1165

Qy   1021 AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT 1080
          |||||||||||||||||||||||||||||     ||||||||||||||| ||||| ||||||
Db   1166 AAAATTCTTTGTGCAACCTACGTGAATGTAAATATTCGAGACATTGATAAGATCTATGTT 1225

Qy   1081 CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1226 CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA 1285

Qy   1141 CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTT 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1286 CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTT 1345

Qy   1201 CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1346 CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA 1405

Qy   1261 GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1406 GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA 1465

Qy   1321 GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1466 GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG 1525

Qy   1381 AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAG 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1526 AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAG 1585

Qy   1441 TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1586 TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC 1645

Qy   1501 AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1646 AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA 1705

Qy   1561 CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1706 CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACA 1765

Qy   1621 CGAAATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC 1680
          |||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db     1766  CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC  1825

Qy     1681  TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT  1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1826  TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT  1885

Qy     1741  AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAGATTGGCCTCCAATCAAACCTGAA  1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1886  AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAGATTGGCCTCCAATCAAACCTGAA  1945

Qy     1801  CAGGCTATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT  1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1946  CAGGCTATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT  2005

Qy     1861  CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA  1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2006  CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA  2065

Qy     1921  CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA  1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2066  CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA  2125

Qy     1981  GCATTGACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCAC  2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2126  GCATTGACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCAC  2185

Qy     2041  AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG  2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2186  AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG  2245

Qy     2101  ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACTTAACT  2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2246  ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACTTAACT  2305

Qy     2161  GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT  2220
             ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db     2306  GACATTCTCAAACAGGAGAAGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT  2365

Qy     2221  GAGCAAATGAGGCGACCAGATTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC  2280
             |||||||||||||||||||||||||||||||||||| ||||||||| |||||||||||||
Db     2366  GAGCAAATGAGGCGACCAGATTTCATGGATGCTCTACAGGGCTTTCTGTCTCCTCTAAAC  2425

Qy     2281  CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAA  2340
             |||||||||||||||||||||||||||||||||||| ||||||||||||||| |||||||
Db     2426  CCTGCTCATCAACTAGGAAACCTCAGGCTTGAAGAGTGTCGAATTATGTCCTCTGCAAAA  2485

Qy     2341  AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC  2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2486  AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC  2545
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Qy    2401  AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT  2460
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2546  AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT  2605

Qy    2461  ATTCGTATTATGGAAAATATCTGGCAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT  2520
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2606  ATTCGTATTATGGAAAATATCTGGCAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT  2665

Qy    2521  GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT  2580
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2666  GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT  2725

Qy    2581  ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA  2640
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2726  ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA  2785

Qy    2641  CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG  2700
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2786  CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG  2845

Qy    2701  TTTACACGTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT  2760
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2846  TTTACACGTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT  2905

Qy    2761  CACAATAGTAACATCATGGTGAAAGACGATGGACAACTGTTTCATATAGATTTTGGACAC  2820
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2906  CACAATAGTAACATCATGGTGAAAGACGATGGACAACTGTTTCATATAGATTTTGGACAC  2965

Qy    2821  TTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG  2880
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2966  TTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG  3025

Qy    2881  ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA  2940
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3026  ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA  3085

Qy    2941  TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT  3000
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3086  TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT  3145

Qy    3001  CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT  3060
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3146  CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT  3205

Qy    3061  GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG  3120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3206  GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG  3265
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Qy      3121 GAGTATTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT 3180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3266 GAGTATTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT 3325

Qy      3181 TGGATCTTCCACACAATTAAACAGCATGCATTGAACTG-AAAGATAACTGAGAAAATGAA 3239
             ||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db      3326 TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAAGATAACTGAGAAAATGAA 3385

Qy      3240 AGCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGC 3299
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3386 AGCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGC 3445

Qy      3300 ATAGGAATTGCACAATCCATGAACAGCATTAG-ATTTACAGCAAGAACAGAAATAAAATA 3358
             |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db      3446 ATAGGAATTGCACAATCCATGAACAGCATTAGAATTTACAGCAAGAACAGAAATAAAATA 3505

Qy      3359 CTATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATT 3418
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3506 CTATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATT 3565

Qy      3419 TCAAAA 3424
             ||||||
Db      3566 TCAAAA 3571
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RESULT 15
ARW65283
ID   ARW65283 standard; cDNA; 3724 BP.
XX
AC   ARW65283;
XX
DT   07-AUG-2008  (first entry)
XX
DE   Human PIK3CA cDNA, SEQ ID 53.
XX
KW   tumor marker; prognosis; diagnostic test; cancer; ss; gene; PIK3CA.
XX
OS   Homo sapiens.
XX
PN   WO2008070325-A2.
XX
PD   12-JUN-2008.
XX
PF   24-OCT-2007; 2007WO-US082397.
XX
PR   26-OCT-2006; 2006US-0863106P.
PR   14-MAY-2007; 2007US-0917814P.
XX
PA   (GETH ) GENENTECH INC.

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XX
PI    Kan Z,  Kenski DM,  Peters B,  Seshagiri S;
XX
DR    WPI; 2008-G69314/42.
DR    P-PSDB; ARW65361.
DR    PC:NCBI; gi54792081.
DR    PC_ENCPRO:NCBI; gi54792082.
XX
PT    New polynucleotide, useful for determining the genotype of a sample from
PT    a mammal, for classifying a tumor in a mammal or for predicting whether a
PT    tumor will respond to a therapeutic agent that targets a PRO polypeptide
PT    or polynucleotide.
XX
PS    Claim 2; SEQ ID NO 53; 98pp; English.
XX
CC    The present invention relates to novel isolated polynucleotides. An
CC    isolated polynucleotide comprises: (a) a PRO polynucleotide or its
CC    fragment that is at least about 10 nucleotides in length or that
CC    comprises a nucleotide variation at a nucleotide position given in the
CC    specification, or (b) its complement. These variations provide biomarkers
CC    for cancer and/or predisposition to tumorigenesis or tumor promotion. The
CC    present invention provides: (1) a kit comprising the oligonucleotide and
CC    at least one enzyme; (2) a microarray comprising the oligonucleotide; (3)
CC    a method for detecting the absence or presence of a nucleotide variation
CC    at a nucleotide position given in the specification, which comprises
CC    contacting the nucleic acid suspected of comprising the nucleotide
CC    variation with an allele-specific oligonucleotide that is specific for
CC    the nucleotide variation and detecting the absence or presence of allele-
CC    specific hybridization; (4) a method for amplifying a nucleic acid
CC    comprising a nucleotide variation at a nucleotide position given in the
CC    specification; (5) a method for determining the genotype of a tumor
CC    sample from a mammal; (6) a method for classifying a tumor in a mammal by
CC    detecting the presence of a variation in a PRO or PRO polynucleotide in a
CC    biological sample derived from the mammal; and (7) a method for
CC    predicting whether a tumor will respond to a therapeutic agent that
CC    targets a PRO or a PRO polynucleotide by determining whether the tumor
CC    comprises a variation in a PRO or PRO polynucleotide, where the presence
CC    of a variation indicates that the tumor will respond to the therapeutic
CC    agent. The method of amplifying a nucleic acid comprising a nucleotide
CC    variation comprises: (a) contacting the nucleic acid with a primer that
CC    hybridizes to the nucleic acid at a sequence 3' of the nucleotide
CC    variation, and (b) extending the primer to generate an amplification
CC    product comprising the nucleotide variation. The variations disclosed in
CC    the invention are useful in methods and compositions related to cancer
CC    diagnosis and therapy. The present sequence is an isolated polynucleotide
CC    of the invention.
CC
CC    Revised record issued on 09-JUL-2008 : Enhanced with precomputed infor
CC
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CC
CC    Revised record issued on 09-JUL-2008 : mation from BOND.
XX
SQ    Sequence 3724 BP; 1242 A; 684 C; 763 G; 1035 T; 0 U; 0 Other;

   Query Match              97.5%;   Score 3338;  DB 7;   Length 3724;
   Best Local Similarity    98.8%;
   Matches 3384;  Conservative    0;  Mismatches   40;  Indels    2;  Gaps    2;


Qy          1 AGGATCAGAACAATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG 60
              || |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db        146 AGAATCAGAACAATGCCTCCACGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG 205

Qy         61 CCCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC 120
              |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db        206 CCCCCAAGAATCCTAGTAGAATGTTTACTACCAAATGGAATGATAGTGACTTTAGAATGC 265

Qy        121 CTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC 180
              |||||||||||||||||| |||| |||||||||||||||||||||||||||||||||||||
Db        266 CTCCGTGAGGCTACATTAATAACCATAAAGCATGAACTATTTAAAGAAGCAAGAAAATAC 325

Qy        181 CCTCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAA 240
              || |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        326 CCCCTCCATCAACTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTTACTCAAGAA 385

Qy        241 GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAA 300
              |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db        386 GCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGACCTTCGGCTTTTTCAA 445

Qy        301 CCATTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA 360
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        446 CCCTTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA 505

Qy        361 ATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTA 420
              ||||||||||||||||||||||||||||||| |||||||||||||||||||||| ||||||
Db        506 ATTGGTTTTGCTATCGGCATGCCAGTGTGTGAATTTGATATGGTTAAAGATCCAGAAGTA 565

Qy        421 CAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTT 480
              |||||||||||||||||||||| || |||||||||||||||||||||||||||||| ||
Db        566 CAGGACTTCCGAAGAAATATTCTGAACGTTTGTAAAGAAGCTGTGGATCTTAGGGACCTC 625

Qy        481 AATTCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG 540
              |||||||||||||||||||||||||||||||||| ||| |||||||||||||||||||||
Db        626 AATTCACCTCATAGTAGAGCAATGTATGTCTATCCTCCAAATGTAGAATCTTCACCAGAA 685

Qy        541 CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTA 600
              |||||||||||||||||||||||| |||| ||| ||||||||||||||||||||| ||||||
Db        686 TTGCCAAAGCACATATATAATAAATTAGATAAAGGGCAAATAATAGTGGTGATCTGGGTA 745
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Qy     601  ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     746  ATAGTTTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTA  805

Qy     661  CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT  720
            |||||||||||||||||||||||||||||||||||||||| ||||||||||||||| |||
Db     806  CCAGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTCGAAGTATGTTGCTATCCTCT  865

Qy     721  GAACAATTAAAACTCTGTGTTTTAGAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGA  780
            ||||||| |||||||||||||||||||||||||||||||||||| |||||||||||||||
Db     866  GAACAACTAAAACTCTGTGTTTTAGAATATCAGGGCAAGTATATTTTAAAAGTGTGTGGA  925

Qy     781  TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT  840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     926  TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT  985

Qy     841  ATAATGCTTGGGAGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAA  900
            ||||||||||||||||||||||||||||||| | ||||||||||||||||||||||||||
Db     986  ATAATGCTTGGGAGGATGCCCAATTTGATGTTGATGGCTAAAGAAAGCCTTTATTCTCAA  1045

Qy     901  CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA  960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1046  CTGCCAATGGACTGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA  1105

Qy     961  TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA  1020
            ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    1106  TATATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGTGCACTCAGAATA  1165

Qy    1021  AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGACAAGATTTATGTT  1080
            |||||||||||||||||||||||||||| |||||||||||||||||| ||||| ||||||
Db    1166  AAAATTCTTTGTGCAACCTACGTGAATGTAAATATTCGAGACATTGATAAGATCTATGTT  1225

Qy    1081  CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA  1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1226  CGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACTCAAAGAGTA  1285

Qy    1141  CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTT  1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1286  CCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCTGATCTT  1345

Qy    1201  CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA  1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1346  CCTCGTGCTGCTCGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA  1405

Qy    1261  GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA  1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1406  GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTA  1465

Qy    1321  GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG  1380
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           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1466  GTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGATTTGCTG 1525

Qy    1381  AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAG 1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1526  AACCCTATTGGTGTTACTGGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAG 1585

Qy    1441  TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC 1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1586  TTTGACTGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC 1645

Qy    1501  AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA 1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1646  AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGA 1705

Qy    1561  CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAGAACAGCTCAAAGCAATTTCTACA 1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1706  CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAGAACAGCTCAAAGCAATTTCTACA 1765

Qy    1621  CGAAATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC 1680
           |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1766  CGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAGACAC 1825

Qy    1681  TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT 1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1826  TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT 1885

Qy    1741  AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAGATTGGCCTCCAATCAAACCTGAA 1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1886  AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAGATTGGCCTCCAATCAAACCTGAA 1945

Qy    1801  CAGGCTATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT 1860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1946  CAGGCTATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT 2005

Qy    1861  CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA 1920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2006  CGGTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTA 2065

Qy    1921  CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA 1980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2066  CAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA 2125

Qy    1981  GCATTGACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCAC 2040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2126  GCATTGACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAATCTGAGATGCAC 2185

Qy    2041  AATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG 2100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db     2186  AATAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGG  2245

Qy     2101  ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACTTAACT  2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2246  ATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACTTAACT  2305

Qy     2161  GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT  2220
             |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db     2306  GACATTCTCAAACAGGAGAAGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT  2365

Qy     2221  GAGCAAATGAGGCGACCAGATTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAAC  2280
             |||||||||||||||||||||||||||||||||| |||||||||| ||||||||||||||
Db     2366  GAGCAAATGAGGCGACCAGATTTCATGGATGCTCTACAGGGCTTTCTGTCTCCTCTAAAC  2425

Qy     2281  CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAA  2340
             ||||||||||||||||||||||||||||||||||| |||||||||||||| |||||||||
Db     2426  CCTGCTCATCAACTAGGAAACCTCAGGCTTGAAGAGTGTCGAATTATGTCCTCTGCAAAA  2485

Qy     2341  AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC  2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2486  AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC  2545

Qy     2401  AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT  2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2546  AATGAGATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT  2605

Qy     2461  ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT  2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2606  ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTAT  2665

Qy     2521  GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT  2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2666  GGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCGAAATTCTCACACT  2725

Qy     2581  ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA  2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2726  ATTATGCAAATTCAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACA  2785

Qy     2641  CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG  2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2786  CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG  2845

Qy     2701  TTTACACGTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT  2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2846  TTTACACGTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGT  2905

Qy     2761  CACAATAGTAACATCATGGTGAAAGACGATGGACAACTGTTTCATATAGATTTTGGACAC  2820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2906  CACAATAGTAACATCATGGTGAAAGACGATGGACAACTGTTTCATATAGATTTTGGACAC  2965
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Qy    2821  TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG  2880
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2966  TTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTG  3025

Qy    2881  ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA  2940
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3026  ACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA  3085

Qy    2941  TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT  3000
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3086  TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAAT  3145

Qy    3001  CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT  3060
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3146  CTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTT  3205

Qy    3061  GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG  3120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3206  GATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTG  3265

Qy    3121  GAGTATTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT  3180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3266  GAGTATTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT  3325

Qy    3181  TGGATCTTCCACACAATTAAACAGCATGCATTGAACTG-AAAGATAACTGAGAAAATGAA  3239
            |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db    3326  TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAAGATAACTGAGAAAATGAA  3385

Qy    3240  AGCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGC  3299
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3386  AGCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGC  3445

Qy    3300  ATAGGAATTGCACAATCCATGAACAGCATTAG-ATTTACAGCAAGAACAGAAATAAAATA  3358
            ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db    3446  ATAGGAATTGCACAATCCATGAACAGCATTAGAATTTACAGCAAGAACAGAAATAAAATA  3505

Qy    3359  CTATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATT  3418
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3506  CTATATAATTTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATT  3565

Qy    3419  TCAAAA  3424
            ||||||
Db    3566  TCAAAA  3571
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Search completed: January 18, 2011, 22:23:11
Job time : 1931 secs
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SCORE 6.0